

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: November 28, 2003, 13:58:18 ; Search time 37.6503 Seconds
(without alignments)
4236.886 Million cell updates/sec

Title: US-09-918-508-4_COPY_32_1036

Perfect score: 5159

Sequence: 1 GIEDKSGLLVGSVDLEKTK.....AEQLYRVSFRFFNSPDSPTES 1005

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1107863 seqs, 158726573 residues

Total number of hits satisfying chosen parameters: 1107863

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

A_Geneseq_19Jun03:*
1: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA1980.DAT.*
2: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA1981.DAT.*
3: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA1982.DAT.*
4: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA1983.DAT.*
5: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA1984.DAT.*
6: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA1985.DAT.*
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14: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA1993.DAT.*
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21: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA2000.DAT.*
22: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA2001.DAT.*
23: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA2002.DAT.*
24: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA2003.DAT.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	5159	100.0	1036	23	ABG70782
2	5159	100.0	1036	24	AA033693
3	5001	96.9	1092	23	AA032567
4	5001	96.9	1092	23	AB991150
5	2685.5	52.1	1132	21	AA047090
6	2685.5	52.1	1176	21	AA047089
7	2685.5	52.1	1176	23	ABG70781
8	2685.5	52.1	1176	24	AA033692
9	2685.5	52.1	1238	21	AA047088

10	2674	51.8	1173	23	AA022568	Wooden leg (WOL) g
11	2674	51.8	1173	23	AB993825	Herbicidally activ
12	2481.5	48.1	1057	23	ABG70783	A. thaliana cytoki
13	2475.5	48.0	1057	23	AA022558	Wooden leg (WOL) g
14	2475.5	48.0	1057	23	AA022570	Wooden leg (WOL) g
15	2475.5	48.0	1057	24	AA033694	Arabidopsis thalia
16	2470.5	47.9	1057	24	AA033696	Arabidopsis thalia
17	2467.5	47.8	1057	24	AA033695	Arabidopsis thalia
18	1487.5	28.8	600	23	AB991688	Herbicidally activ
19	975	18.9	412	21	AA025530	Eucalyptus grandis
20	937.5	18.2	426	21	AA025516	Eucalyptus grandis
21	867.5	16.8	274	23	AA022561	Wooden leg (WOL) g
22	849.5	16.5	289	23	AA022563	Wooden leg (WOL) g
23	884.5	13.3	1238	19	AA068522	Wooden leg (WOL) g
24	684.5	13.3	1298	20	AA022561	N. crassa osp pro
25	682.5	13.2	1281	20	AA022561	osl-p amino acid s
26	682.5	13.2	1281	20	AA022561	osl histidine kina
27	651	12.6	1018	21	AA025534	osl histidine kina
28	640.5	12.4	1081	20	AA022561	Eucalyptus grandis
29	640.5	12.4	1081	20	AA022561	cos-1 histidine ki
30	620.5	12.0	922	22	AA022566	Candida albicans C
31	620.5	12.0	922	22	AA022566	Histidine protein k
32	615.5	11.9	922	22	AA022566	Histidine protein k
33	600	11.6	170	21	AA025148	Eucalyptus grandis
34	594.5	11.5	950	23	AB993422	Herbicidally activ
35	563	10.9	2150	23	AA022566	Wooden leg (WOL) g
36	560	10.9	971	20	AA088480	Candida albicans h
37	560	10.9	2471	20	AA088481	Candida albicans h
38	557.5	10.8	1122	23	AB992150	Herbicidally activ
39	543	10.5	816	21	AA025508	Eucalyptus grandis
40	534.5	10.4	666	24	AA026994	Pseudomonas aerugi
41	534.5	10.4	709	24	AA026993	Pseudomonas aerugi
42	534.5	10.4	719	24	AA026992	Pseudomonas aerugi
43	534.5	10.4	802	24	AA026991	Pseudomonas aerugi
44	534.5	10.4	870	24	AA026990	Pseudomonas aerugi
45	534.5	10.4	874	24	AA026989	Pseudomonas aerugi

ALIGNMENTS

RESULT 1

ABG70782
ID ABG70782 standard; Protein; 1036 AA.

AC ABG70782;

XX XX

XX 09-DEC-2002 (first entry)

DT XX

DE A. thaliana cytokinin receptor, AHK3, protein.

XX AHK3; plant; antagonist; agonist; cytokinin receptor;

KW receptor; signal transduction; histidine kinase; hormone; cell division;

XX cell differentiation; agriculture; growth regulator; harvest.

XX OS Arabidopsis thaliana.

XX FH Key

FT Region

FT Location/Qualifiers

FT 32..1036

FT /note= "This region is specifically claimed in Claim 1"

XX EP1241182-A2.

XX 18-SEP-2002.

XX 13-MAR-2002; 2002EP-0005749.

XX 15-MAR-2001; 2001JP-0073812.

PR 29-JUN-2001; 2001JP-0198639.

PR 29-JUN-2001; 2001JP-0198640.

XX A. thaliana cytoki

PA Arabidopsis thalia

XX Arabidopsis thalia

XX (SUMO) SUMITOMO CHEM CO LTD.

Kakimoto T, Higuchi M, Inoue T;
 WI; 2002-693041/75.
 N-PSDS; ABS54451.

Analyzing agonist or antagonist activity of a substance for use as a plant growth regulator, comprises measuring intracellular signal transduction from a cytokinin receptor expressed in a cell contacted with the test substance -

Claim 1; Page 32-34; 47pp; English.

The invention discloses a method for analysing antagonist or agonist activity to a cytokinin receptor. The method comprises bringing a candidate substance into contact with a transformed cell, in which a DNA encoding the receptor has been introduced, and then measuring the existence, or the quantity, of the intracellular signal transduction from the receptor expressed in the cell. The cytokinin receptor comprises an extracellular region of the receptor, transmembrane regions, a histidine kinase region and a receiver region of the kinase. The transmembrane regions and kinase region are homogeneous to each other and the receptor region is heterogeneous to them. Cytokinins are plant hormones relevant to cell division and differentiation of higher plants. The method is used for analysing agonist or antagonist activity to a cytokine receptor. A substance with agonist or antagonist activity to the receptor can be used, in agriculture, as a plant growth regulator, e.g. after harvest. The advantage is that the candidate substances do not need to be prepared in such large amounts as in previous methods and that the method avoids the immensely long time to observe and evaluate the growth of the plant and the physiological changes of the plant after spraying. The sequence presented is the A. thaliana cytokinin receptor, AHK3, protein.

Sequence 1036 AA;

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Query          100.0%; Score 5159; DB 23; Length 1036;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1005; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY   1  GIEDKSGLLVGSGDLEKTWTLTKKNKMWFWNKKISSSGLKIPFSYQFLGSVFNKAW 60
DB   32  GIEDKSGLLVGSGDLEKTWTLTKKNKMWFWNKKISSSGLKIPFSYQFLGSVFNKAW 91

QY   61  WRKLVVVVVWVLVSIWTFFWSSQAMEKRKETLASMCDERARMLQDFNVSMNHVOAM 120
DB   92  WRKLVVVVVWVLVSIWTFFWSSQAMEKRKETLASMCDERARMLQDFNVSMNHVOAM 151

QY  121  SILISTFHGKIISAIDORTFSEYTDRTSPERPLTSGVAYMRVLHSEEBEEROOGWTI 180
DB  152  SILISTFHGKIISAIDQRTFSEYTDRTSPERPLTSGVAYMRVLHSEEBEEROOGWTI 211

QY  181  RKMYSLEQNPHVKDDXDLEALEPVEEQEEYAPVIFAQDTVSHVVSIDMLSGKEDRENVL 240
DB  212  RKMYSLEQNPHVKDDYDLEALEPVEEQEEYAPVIFAQDTVSHVVSIDMLSGKEDRENVL 271

QY  241  ARSGKGVLTPAPPLIKTNRLGVILTFVAVKYRDLPSNATPKRIEATNGYLGGVFIESL 300
DB  272  ARSGKGVLTPAPPLIKTNRLGVILTFVAVKYRDLPSNATPKRIEATNGYLGGVFIESL 331

QY  301  VENLLQOLASKQTILVNVDITNHSOPISMYGTVNSADGLERVSLIFGDPLRKHEMCRCR 360
DB  332  VENLLQOLASKQTILVNVDITNHSOPISMYGTVNSADGLERVSLIFGDPLRKHEMCRCR 391

QY  361  FKQKPPMPVLISMTVSFGILVIALVAHIHATVSRILHKVEEDCKMKQLKKAEAAADVAK 420
DB  392  FKQKPPMPVLISMTVSFGILVIALVAHIHATVSRILHKVEEDCKMKQLKKAEAAADVAK 451

QY  421  SQFIATVSHIRTPMGVGLMHLMDTELDTVTQQDYVRTAQASGKALVSLINEVLDOAK 480
DB  452  SQFIATVSHIRTPMGVGLMHLMDTELDTVTQQDYVRTAQASGKALVSLINEVLDOAK 511

QY  481  IESKLELEVRFDRGLIDDVLSLFSSSQOKGVELAVVISDRVDPMLIGPGFRQILL 540
DB  512  IESKLELEVRFDRGLIDDVLSLFSSSQOKGVELAVVISDRVDPMLIGPGFRQILL 571

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CC response regulator operably linked to a promoter functional in plant
CC cells to yield transformed plant cells or whose expression reduces the
CC expression of A-type response regulator in the cells of the plant and
CC regenerating a plant from the transformed cells. The method is useful
CC for increasing the yield in a plant, increasing the shoot formation or
CC delaying senescence in a plant such as wheat, rice, maize, barley,
CC potato, tomato, soybean, oat, cotton and sunflower. The method
CC is useful for variety of agricultural and commercial purposes including
CC improving and enhancing photosynthesis, promoting cell proliferation,
CC shoot meristem formation, promoting leaf development, increasing crop
CC yield, improving crop and ornamental quality and reducing agricultural
CC production costs. The present sequence is Arabidopsis thaliana histidine
CC kinase 3 (AHK3) protein. This sequence is used to illustrate the method
CC of the invention.

XX
SQ Sequence 1036 AA;

Query Match 100.0%; Score 5159; DB 24; Length 1036;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1005; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GIEDKSGLLVGSVGLDKTKMTTLKKNKMFNWKISSGLKIPFSYQFLGSKFNKAW 60
Db 32 GIEDKSGLLVGSVGLDKTKMTTLKKNKMFNWKISSGLKIPFSYQFLGSKFNKAW 91
Qy 61 WRKLVVVVFWVLVSIWTFYSSQAMERKKTLSMCDERARMLQDQFNVSNNHVQAM 120
Db 92 WRKLVVVVFWVLVSIWTFYSSQAMERKKTLSMCDERARMLQDQFNVSNNHVQAM 151
Qy 121 SILISTPHHGKIPSAIDQRTFSEYDTRTSRPLTSGVAVAMRVLHSEFEFEQQGWTI 180
Db 152 SILISTPHHGKIPSAIDQRTFSEYDTRTSRPLTSGVAVAMRVLHSEFEFEQQGWTI 211
Qy 181 RMYSLQNPHKDDYDLEALPSPQVEEYAPVIFAQDTVSHVSLDMLSGKEDRENVL 240
Db 212 RMYSLQNPHKDDYDLEALPSPQVEEYAPVIFAQDTVSHVSLDMLSGKEDRENVL 271
Qy 241 ARSSGKGVLTAPPFLIKTNRLGVILTFAVYKRDLPNSNATPKERIEATNGYLGVDIESL 300
Db 272 ARSSGKGVLTAPPFLIKTNRLGVILTFAVYKRDLPNSNATPKERIEATNGYLGVDIESL 331
Qy 301 VENLLOQASQOTILVNVYDITNHSQPSIMVGTWVSADGLERSVPLIFGDPPLKHENRCR 360
Db 332 VENLLOQASQOTILVNVYDITNHSQPSIMVGTWVSADGLERSVPLIFGDPPLKHENRCR 391
Qy 361 FKQKPPMPVLSMTSFGILVIALVAHIIEATVSRHKEVEDCDKMKQLKKAADAVAK 420
Db 392 FKQKPPMPVLSMTSFGILVIALVAHIIEATVSRHKEVEDCDKMKQLKKAADAVAK 451
Qy 421 SQFLATVSHETRTPMNGVGLMMLMDTELDTQDYVVRTAQASGKALVSLINEVLDOAK 480
Db 452 SQFLATVSHETRTPMNGVGLMMLMDTELDTQDYVVRTAQASGKALVSLINEVLDOAK 511
Qy 481 IESGKLEEVREDLIGLDVLSLFSKSKQOKGVELAVISDRVPMMLIGDPRPQIL 540
Db 512 IESGKLEEVREDLIGLDVLSLFSKSKQOKGVELAVISDRVPMMLIGDPRPQIL 571
Qy 541 TNLMGNSIKTEKGHIFVTVHVLVDELPESDIGETASSPESTLSGLPVADRQSRWENFKAF 600
Db 572 TNLMGNSIKTEKGHIFVTVHVLVDELPESDIGETASSPESTLSGLPVADRQSRWENFKAF 631
Qy 601 SSNGHRFSPSPDINILVSVEDTGVGIPVEAQSRIFTFPMQVGPSISRTHGFTGIGLSI 660
Db 632 SSNGHRFSPSPDINILVSVEDTGVGIPVEAQSRIFTFPMQVGPSISRTHGFTGIGLSI 691
Qy 661 SKCLVGLMKGEIGFSSSTPKVGTSTFTTAVFSNGQPAERKNDNNQPIFSFRGKAVYVD 720
Db 692 SKCLVGLMKGEIGFSSSTPKVGTSTFTTAVFSNGQPAERKNDNNQPIFSFRGKAVYVD 751
Qy 721 HRPARAKVSWTHFORLIGRVEVPRVFOALHYLKIGTTTVMMLIEQIWNREADDFIKK 780
Db 752 HRPARAKVSWTHFORLIGRVEVPRVFOALHYLKIGTTTVMMLIEQIWNREADDFIKK 811

Qy 781 LOKDPLFLSPKLLILANSVSESSISEALCTGIDPPIVIVKPLRSMLAATLQGLGIGIRE 840
Db 812 LQKDPFLFLSPKLLILANSVSESSISEALCTGIDPPIVIVKPLRSMLAATLQGLGIGIRE 871
Qy 841 PPQHKGPAPALILRNLLIGRKLILVDDNNVNLRLVAAGALKKYGADVVCAESSGIKAILLKP 900
Db 872 PPQHKGPAPALILRNLLIGRKLILVDDNNVNLRLVAAGALKKYGADVVCAESSGIKAILLKP 931
Qy 901 PHFDFACFMDIQMPMDGFEATRIRIDMBEEMNKRKNGEALIVENGKNTSWHLPLVLAAMT 960
Db 932 PHFDFACFMDIQMPMDGFEATRIRIDMBEEMNKRKNGEALIVENGKNTSWHLPLVLAAMT 991
Qy 961 ADVIQATHEECLKCGMDGVYVSKPFEAEQLYREVSRFNSPDSDES 1005
Db 992 ADVIQATHEECLKCGMDGVYVSKPFEAEQLYREVSRFNSPDSDES 1036

RESULT 3
AAO22567
ID AAO22567 standard; Protein; 1092 AA.
XX
AC AAO22567;
XX
DT 28-OCT-2002 (first entry)
XX
DE Wooden leg (WOL) gene related protein SEQ ID No 18.
XX
KW Wooden leg; WOL; vasculature; transgenic plant; agronomic; longer root;
XX wood production; plant; promoter; tree; crop plant.
XX Arabidopsis thaliana.
XX
PN WO200244337-A2.
XX
PD 06-JUN-2002.
XX
PF 29-NOV-2001; 2001WO-US45053.
XX
PR 29-NOV-2000; 2000US-253739P.
XX
PA (UNY) UNIV NEW YORK STATE.
PA (HELA/) HELARIUTTA Y.
PA (MAHO/) MAHONEN A P.
PA (BONK/) BONKE A W M.
PA (KAUP/) KAUPPINEN L.
PA (RIIK/) RIIKONEN M.
XX
PI Helariutta Y, Mahonen AP, Bonke AWM, Kauppinen L, Riikonen M;
PI Benfey PN;
XX
DR WPI; 2002-599423/64.
XX
PT Novel isolated polypeptide (WOODEN LEG) with ability to regulate a set
PT of asymmetric cell divisions that establish vascular tissue in root and
PT hypocotyl development, useful for improving agronomically valuable
PT plants -
XX
PS Example 1; Page 157-161; 187pp; English.
XX
CC The invention relates to an isolated WOODEN LEG (WOL) polypeptide,
CC comprising 15 contiguous amino acids of a fully defined Arabidopsis
CC WOODEN LEG protein sequence of 1057 amino acids as given in the
CC specification, and to its encoding nucleic acid. The invention also
CC relates to an amino acid sequence of domains of protein, e.g., N-terminal
CC region, C-terminal domain, etc; or is a naturally occurring allelic
CC variant of the above mentioned polypeptide sequence. Expression levels of
CC the nucleic acid can be modified to improve the vasculature in transgenic
CC plants and enhance the agronomic properties of such plants. Also the WOL
CC promoter is used to drive expression of a heterologous coding sequence of
CC trees to improve wood production. The WOL nucleic acid may be used as a
CC molecular marker for a qualitative trait loci, e.g., longer roots or
CC enhanced wood production, in molecular breeding of crop plants. The
CC nucleic acid is also useful in DNA amplification assays to identify the

CC endogenous WOL genes, WOL mutant alleles and/or WOL expression products
CC in cultivars as compared to wild-type plants. They can also be used as
CC markers for linkage analysis of qualitative trait loci. The WOL protein
CC and/or antibodies can be used as diagnostic reagents in immunoassays to
CC detect expression of the WOL gene in cultivars and wild-type plants. The
CC WOL protein, its encoding nucleic acid, and its corresponding antibody
CC are useful for improving agronomically valuable plants e.g., trees. This
CC sequence represents a protein relating to the wooden leg (WOL) protein of
CC the invention.

XX	Sequence	1092 AA;	
Query Match	96.9%;	Score 5001;	DB 23; Length 1092;
Best Local Similarity	96.8%;	Pred. No. 0;	
Matches	979;	Conservative	0; Mismatches 0; Indels 32; Gaps 1;
QY	1	GIEDKSGLLVSGDLEKTKMTTLKKKNKMFNWKISSGLKIPSPSYQFLGSVKFNKAW	60
Db	32	GIEDKSGLLVSGDLEKTKMTTLKKKNKMFNWKISSGLKIPSPSYQFLGSVKFNKAW	91
QY	61	WRKLVVVVWVFWVLVSIWTFWYFSSQAMEKREKTELASMCDEARMLQDQFNVMNHVQAM	120
Db	92	WRKLVVVVWVFWVLVSIWTFWYFSSQAMEKREKTELASMCDEARMLQDQFNVMNHVQAM	151
QY	121	SILISTFHGKIPSAIDQRTFSEYTDRTSPERPLTSGVAYAMRVLHSEREPERQCGWTI	180
Db	152	SILISTFHGKIPSAIDQRTFSEYTDRTSPERPLTSGVAYAMRVLHSEREPERQCGWTI	211
QY	181	RKMSLEQNPVHKDDYDLALPSPVQBEYAPVIFAQDVTSHVVSIDMLSGKEDRENVL	240
Db	212	RKMSLEQNPVHKDDYDLALPSPVQBEYAPVIFAQDVTSHVVSIDMLSGKEDRENVL	271
QY	241	ARSSGKGVLTAPPLIKTNRLGVILTFVAYKRDLPNSATPKERIEATNGYLGVDIESL	300
Db	272	ARSSGKGVLTAPPLIKTNRLGVILTFVAYKRDLPNSATPKERIEATNGYLGVDIESL	331
QY	301	VENLLQOLASKOTILVNVYDITNHSQIPSMYGTNVSADGLERSVPLIFGDPLRKHEMR	358
Db	332	VENLLQOLASKOTILVNVYDITNHSQIPSMYGTNVSADGLERSVPLIFGDPLRKHEMR	391
QY	359	-----CEFKQPPWVLVSMYTSFGIILVALLVAHI	388
Db	392	YLOLAHYVCNFFLPARIQVLFCCELLPLCPKPKPPWVLVSMYTSFGIILVALLVAHI	451
QY	389	IHATVSRIRHKVEDCDKMKQKKKAAADVAKSQFLATVSHVSHVSHVSHVSHVSHVSHV	448
Db	452	IHATVSRIRHKVEDCDKMKQKKKAAADVAKSQFLATVSHVSHVSHVSHVSHVSHVSHV	511
QY	449	ELDVTQDDVVRTAQASGKALVSLINEVLDQAKIESGKLEEVREDFLRGILDVLSLFS	508
Db	512	ELDVTQDDVVRTAQASGKALVSLINEVLDQAKIESGKLEEVREDFLRGILDVLSLFS	571
QY	509	KSQQGVVELAVVSDRVPDMLGDCRFRQIILTNLMGNSIKTEKGHIFVTVHLDVLEFE	568
Db	572	KSQQGVVELAVVSDRVPDMLGDCRFRQIILTNLMGNSIKTEKGHIFVTVHLDVLEFE	631
QY	569	SIDGETASSPESTLSGLPVADQRSWENFKAFSSNGHRSFSPSPDINLIVSEDTGVGI	628
Db	632	SIDGETASSPESTLSGLPVADQRSWENFKAFSSNGHRSFSPSPDINLIVSEDTGVGI	691
QY	629	PVEAQSRIPTPMQVGPISIRHTGGTIGLSISKVLGMLKGEIGFSPSTPKVGSFTTFTA	688
Db	692	PVEAQSRIPTPMQVGPISIRHTGGTIGLSISKVLGMLKGEIGFSPSTPKVGSFTTFTA	751
QY	689	VFSNGMOPAEKNDNNQPIFSEFRGMKAVVDHPRAPAKVSNYHQRGIRVEVPRVEQ	748
Db	752	VFSNGMOPAEKNDNNQPIFSEFRGMKAVVDHPRAPAKVSNYHQRGIRVEVPRVEQ	811
QY	749	ALHYLKIGTTVMILLIEQIENRADDPIKQLQDPLFLSKILLANSVSSISSEALC	808
Db	812	ALHYLKIGTTVMILLIEQIENRADDPIKQLQDPLFLSKILLANSVSSISSEALC	871
QY	809	TGIDPPFIVIVKPLRASMLAATLQRLGIGIREPPQHKGPALILNLLGRKILIVDDNN	968

Db	872	TGIDPPFIVIVKPLRASMLAATLQRLGIGIREPPQHKGPALILNLLGRKILIVDDNN	931
QY	869	VNLRVAAGALKKYGADVVCASGIIKAIISLKKPPHFDACFWDIOMPENWDGFEATRIRDM	928
Db	932	VNLRVAAGALKKYGADVVCASGIIKAIISLKKPPHFDACFWDIOMPENWDGFEATRIRDM	991
QY	929	EENMKRIKNGEALIVENGKTSWHLPLVAMTADVIQATHEBCLKCGMDGY	979
Db	992	EENMKRIKNGEALIVENGKTSWHLPLVAMTADVIQATHEBCLKCGMDGY	1042

RESULT 4			
ABB91150	ID	ABB91150 standard; Protein; 1092 AA.	
XX	AC	ABB91150;	
XX	XX	31-MAY-2002 (first entry)	
XX	DE	Herbicide active polypeptide SEQ ID NO 361.	
XX	KW	Herbicide; plant; agriculture; herbicide.	
XX	OS	Arabidopsis thaliana.	
XX	PN	WO200210210-A2.	
XX	PD	07-FEB-2002.	
XX	PF	28-AUG-2001; 2001WO-EP09892.	
XX	PR	28-AUG-2001; 2001WO-EP09892.	
XX	PA	(FARB) BAYER AG.	
XX	PI	Tietjen K, Weidler M;	
XX	DR	WPI; 2002-269010/31.	
XX	PT	Identifying plant target proteins for herbicidally active compounds, comprising aligning and comparing nucleic acid or amino acid sequences from plant with nucleic acid or amino acid sequences from non-plant organisms -	
XX	PS	Claim 5; SEQ ID NO 361; 261pp + Sequence Listing; English.	
XX	CC	The invention relates to identifying target proteins (ABB90790-ABB94016) for herbicidally active compounds, comprising aligning and comparing nucleic acid or amino acid sequences from plant with nucleic acid or amino acid sequences from non-plant organisms using suitable search parameters, where plant sequences having an E-value greater by a factor of 3 than the E-value of most similar non-plant sequences are selected. The polypeptides or nucleic acids encoding them are useful for identifying modulators. The identified modulators are useful as herbicides.	
XX	SQ	Sequence 1092 AA;	

Query Match	96.9%;	Score 5001;	DB 23; Length 1092;
Best Local Similarity	96.8%;	Pred. No. 0;	
Matches	979;	Conservative	0; Mismatches 0; Indels 32; Gaps 1;
QY	1	GIEDKSGLLVSGDLEKTKMTTLKKKNKMFNWKISSGLKIPSPSYQFLGSVKFNKAW	60
Db	32	GIEDKSGLLVSGDLEKTKMTTLKKKNKMFNWKISSGLKIPSPSYQFLGSVKFNKAW	91
QY	61	WRKLVVVVWVFWVLVSIWTFWYFSSQAMEKREKTELASMCDEARMLQDQFNVMNHVQAM	120
Db	92	WRKLVVVVWVFWVLVSIWTFWYFSSQAMEKREKTELASMCDEARMLQDQFNVMNHVQAM	151
QY	121	SILISTFHGKIPSAIDQRTFSEYTDRTSPERPLTSGVAYAMRVLHSEREPERQCGWTI	180

Db	152	SILISTFHGKIPSAIQDRTSFSEYTDRTSFERPLTSGVAYAMRVLHRSEREEFERQGGWTI	211	OS	Arabidopsis thaliana.
Qy	181	RMVSLQNPVHKDDYDLEALPSPVQBEYAPVITFAQDTVSHVSLDMLSGKEDRENVL	240	XX	EP1033405-A2.
Db	212	RMVSLQNPVHKDDYDLEALPSPVQBEYAPVITFAQDTVSHVSLDMLSGKEDRENVL	271	XX	06-SEP-2000.
Qy	241	ARSSGKGVLTAPFPIIKTNRLGVILTFVAYKRDLPNSNATPKERIEATNGYLGGVDFISL	300	PF	25-FEB-2000; 2000EP-0301439.
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Qy	301	VENLIQQLASKQITLVNVDITNHSQPISMYGTNVSADGLERVSPLIFGDPPLRKHEMR	--	PR	25-FEB-1999; 99US-0121825.
Db	332	VENLIQQLASKQITLVNVDITNHSQPISMYGTNVSADGLERVSPLIFGDPPLRKHEMR	391	PR	05-MAR-1999; 99US-0123180.
Qy	359	-----CRFKOKPPWPVLVSMVTSFGIILVIALVAHI	388	PR	09-MAR-1999; 99US-0123548.
Db	392	YIQLAHTVVCNFFLFARIQVLPFCCELLPLCFKQKPPWPVLVSMVTSFGIILVIALVAHI	451	PR	23-MAR-1999; 99US-0125788.
Qy	389	IHATVSRHKHVEDCDKKQLKKKBAADVAKSQFLATVSHIETPMNGVLGMLHMLMDT	448	PR	25-MAR-1999; 99US-0126264.
Db	452	IHATVSRHKHVEDCDKKQLKKKBAADVAKSQFLATVSHIETPMNGVLGMLHMLMDT	511	PR	29-MAR-1999; 99US-0126785.
Qy	449	ELDVTQDDYVRTAQASGKALVSLINEVLDQAKIESGKLEBEVRFDLRLGILDDVLSLFS	508	PR	01-APR-1999; 99US-0127462.
Db	512	ELDVTQDDYVRTAQASGKALVSLINEVLDQAKIESGKLEBEVRFDLRLGILDDVLSLFS	571	PR	06-APR-1999; 99US-0128234.
Qy	509	KSQQKGVELAVVISRVPDMLIGDGRFRQILTNLMGNSIKPTEKGHIFVTVHLVDELFE	568	PR	08-APR-1999; 99US-0128714.
Db	572	KSQQKGVELAVVISRVPDMLIGDGRFRQILTNLMGNSIKPTEKGHIFVTVHLVDELFE	631	PR	16-APR-1999; 99US-0129845.
Qy	569	SIDGETASSPSTLSGLPVADRQRWENFKAFSSNGHSPSPDPDNLIVSVEDTGVI	628	PR	19-APR-1999; 99US-0130077.
Db	632	SIDGETASSPSTLSGLPVADRQRWENFKAFSSNGHSPSPDPDNLIVSVEDTGVI	691	PR	21-APR-1999; 99US-0130449.
Qy	629	PVEAQSRIFTFPMQVGPSISRTHGTTGIGLSISKLVGLMKGEIGFSSTPKVGVSTFTFTA	688	PR	23-APR-1999; 99US-0130510.
Db	692	PVEAQSRIFTFPMQVGPSISRTHGTTGIGLSISKLVGLMKGEIGFSSTPKVGVSTFTFTA	751	PR	28-APR-1999; 99US-0130891.
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Db	752	VFSNGMQPAERKNNQDPIFSEFRGMKAVVDHRRPARAKVSWYHFQRLGIRVEVVPRVEQ	811	PR	04-MAY-1999; 99US-0132048.
Qy	749	ALHYLKIGTTVMMLIEQETWNRADDPIKKLOKPLFLSPKILLANSVSSISEALC	808	PR	05-MAY-1999; 99US-0132484.
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Qy	869	VNLRAAGALKKYGADVVCBSGKIKALSLLKPPHEFDACFMDIQMPMDGFEATRIRDM	928	PR	14-MAY-1999; 99US-0134256.
Db	932	VNLRAAGALKKYGADVVCBSGKIKALSLLKPPHEFDACFMDIQMPMDGFEATRIRDM	991	PR	14-MAY-1999; 99US-0134218.
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XX	hybridisation assay; generic mapping; gene expression control; promoter;				99US-0137724.
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Query Match 52.1%; Score 2685.5; DB 21; Length 1132;
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Matches 551; Conservative 142; Mismatches 224; Indels 47; Gaps 13;

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QY 120 MSILITSTPHHGKIPSAIDORTFSEYTDRTSPERPLTSGVAYAMRVLHSEREFEERQOQWT 179
Db 246 LSLIVSTFHHGKIPSAIDORTFSEYTERTNFERPLTSGVAYALKVPHSERKFKFEHGA 305

QY 180 IRKMYSLQNPVHKDDYDLEALPSPVOEYAPVIFAQDTVSHVVSJDLMSGKEDRENVL 239
Db 306 IKKMETEDQTVV--QDCVPENFDPAIQDEYAPVIFAQETVSHIVSVDMMSGEEDRENIL 363

QY 240 RARSGKGLTAPPLTKTNELGVILFVYKRDLPNATPKERIEATNGYLGGVFOIES 299
Db 364 RARASGKGLTSPFKLLKSNHLGVILFVYVDTSLPPDATBEQRVEATIGYLASDYDMP 423

QY 300 LVENLLQOLASKQITLVNVYDITNHSQPISMYGTNVSADGLERVSPILIFGDPPLKHEMRC 359
Db 424 LVEKLLQLASKQITADVVDYDITNHSGLIKMYGEIGDISEQHILSSJDFGDPSPRHEMHC 483

QY 360 RFKOKPPWVLSMVSFGLIVALLVAHIIHATVSRHKVEEDCDKMKQLKKAFAADVA 419
Db 484 RFKHKLPIPWTAITPSILVLVITELVGYILVEALNRATVEEDCQKRELKARAFADIA 543

QY 420 KSOFLATVSHIRTPMNGVLGNHMLMDTELDVTDQDYVTRTAQASGKALVSLINEVDQA 479
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QY 589 DQRGSWENPK-AFSSNGHRSFPSPDPINLIIVSVEDTGVGIVFEAQSRIFTFFPMQVGPFI 647
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QY 708 -----FSFRGMKAVVVDHRRPARAKVSVYHFQRLGIRVEVVPVREQALHLYLKIGTT 758
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DT 18-OCT-2000 (first entry)
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KW Protein identification; signal transduction pathway; metabolic pathway;
KW hybridisation assay; genetic mapping; gene expression control; promoter;
KW termination sequence.
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OS Arabidopsis thaliana.
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AC ABG70781;
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DT 09-DEC-2002 (first entry)
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DE A. thaliana cytokinin receptor, AHK2, protein.
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KW AHK2; plant; antagonist; agonist; cytokinin receptor;
KW receptor; signal transduction; histidine kinase; hormone; cell division;
KW cell differentiation; agriculture; growth regulator; harvest.
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OS Arabidopsis thaliana.
XX
FH Key
FT Location/Qualifiers
FT Region
FT /note= "This region is specifically claimed in Claim 1"
FT 196..1176
FT /note= "This region is specifically claimed in Claim 1"
XX
PN EPI241182-A2.
XX
PD 18-SEP-2002.
XX
PF 13-MAR-2002; 2002EP-0005749.
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PR 15-MAR-2001; 2001JP-0073812.
PR 29-JUN-2001; 2001JP-0198639.
PR 29-JUN-2001; 2001JP-0198640.
XX
PA (SUMO) SUMITOMO CHEM CO LTD.
XX
PI Kakimoto T, Higuchi M, Inoue T;
XX
DR WPI; 2002-693041/75.
DR N-PSDB; ABS54450.
XX
XX Analyzing agonist or antagonist activity of a substance for use as a
PT plant growth regulator, comprises measuring intracellular signal
PT transduction from a cytokinin receptor expressed in a cell contacted
PT with the test substance -
XX
PS Claim 1; Page 26-28; 47pp; English.
XX

CC The invention discloses a method for analysing antagonist or agonist
CC activity to a cytokinin receptor. The method comprises bringing a
CC candidate substance into contact with a transformed cell, in which a DNA
CC encoding the receptor has been introduced, and then measuring the
CC existence, or the quantity, of the intracellular signal transduction from
CC the receptor expressed in the cell. The cytokinin receptor comprises an
CC extracellular region of the receptor, transmembrane regions, a histidine
CC kinase region and a receiver region of the kinase. The transmembrane
CC regions and kinase region are homogeneous to each other and the receptor
CC region is heterogeneous to them. Cytokinins are plant hormones relevant
CC to cell division and differentiation of higher plants. The method is used
CC for analysing agonist or antagonist activity to a cytokine receptor. A
CC substance with agonist or antagonist activity to the receptor can be
CC used, in agriculture, as a plant growth regulator, e.g. after harvest.
CC The advantage is that the candidate substances do not need to be prepared
CC in such large amounts as in previous methods and that the method avoids
CC the immensely long time to observe and evaluate the growth of the plant
CC and the physiological changes of the plant after spraying. The sequence
CC presented is the A. thaliana cytokinin receptor, AHK2, protein.
XX

SQ Sequence 1176 AA;

Query Match 52.1%; Score 2685.5; DB 23; Length 1176;
Best Local Similarity 57.2%; Pred. No. 1.2e-222;
Matches 551; Conservative 142; Mismatches 224; Indels 47; Gaps 13;

QY 61 WRK-LVVVVVFWVLVSIWTFYFSSQAMEKREKTELASCMCDERARMLQDQFNVMNHVQA 119
Db 230 WRKNILLGILGGVSFVFWFDNTEIIMKRRTLANMCDERARVLQDQFNVLNHVHA 289
QY 120 MSILISTFHGKIPSAIDQRTFSEYDTRTSPERPLTSGVAYAMRVLSREEFERQOGWT 179
Db 290 LSLIVSTFHGKIPSAIDQRTFSEYDTRTSPERPLTSGVAYALVPHSREKPEKHGWA 349
QY 180 IRKWSLEQNPVHKDDYDLALPSPVOEYAPVIFAQDTVSHVSLDMLSGKEDRENVL 239
Db 350 IKMETEDQTVV--QDCVPENFOPAPIQDEYAPVIFAQTVSHVSVVDMMSGEEDRENIL 407
QY 240 RARSGGKVLTAPEPLIKTNRLGVLITFAVVKRDLPSNATPKERIATNGVLGVFFDIES 299
Db 408 RARAGKVLTSFPLKLSNHLGVLTFAVYDTSLLPDATEEQREATEIGVLGASYDMP 467
QY 300 LVENLLOOLASKOTILVNVYDITNHSQPISMYGTNVVSADGLERSPLIFGDLRKHMR 359
Db 468 LVKELLHQLASKOTIAVDVYDTTNTSLIKMYGSEIGDISEQHSLSLDFDPSNEMHC 527
QY 360 RFKQKPPVPLSVMTSPGIIIVLAHIIHATVSRTHKVEEDCDKMKQLKKAADVA 419
Db 528 RFKHLKPIPWTAITPSILVITFLVGYILYEAINRIATVTEEDCQKRELKARAAADIA 587
QY 420 KSQFLATVSHEIRTPMNGVLGMLHMLMDTELDVTQDDYVTRTAQASGKALVSLINEVLDOA 479
Db 588 KSQFLATVSHEIRTPMNGVLGMLXMLMDTDLAKQMDYAGTARGSGKDLTSLINEVLDOA 647
QY 480 KIESGKLEEEVDFDLRGILLDDVLFSKSKQKGVELAVIISDRVDPMLIGPGRFQI 539
Db 648 KIESGRLEENVPDMRFILDNVSSLLSGKANEKIELAVYVSSQVDPVVVGPSPRQI 707
QY 540 LTNLMGNSIKFT-EKGHIFVTYVHLVDLPESIDGETA-----SSPESTLSGLPVA 588
Db 708 ITNLVGNISIKFTQERGHIFISVHLADEVREPLTIEDAVLKQRLALGCSGSETVSGPPAV 767
QY 589 DRQSWENPK-AFSSNGHRSFSPDPDINLIVSVEDTGVGPVEAQSRFTTPMQVGP 647
Db 768 NAWGSMWNFKCYSTESQNS-----DQIKLVTVEDTGVGPVDAQGRIFTTPMQADSST 822
QY 648 SRTHGTGIGLSISKLVGLMKGEIGFSSTPKVGSSTFTTAVFSGMQPAERKNDNNQPI 707
Db 823 SRTYGGTIGLISIKRLVELMQEMGVSEPGIGSTFSFTGVFG-----KAETNTSI 874
QY 708 -----FSEFRGMKAVVDHRRARAKVSYHYHQRLGIRVEVVRVEQALHYLKIGTT 758
Db 875 TKLERFDLAIQFTGLRALVIDNRNIRAEVTRYELRIGISADIVSSLRMACTCISKLE 934

QY 994 SREF 997
Db 1170 ARFF 1173

RESULT 9
AAG47088
ID AAG47088 standard; Protein; 1238 AA.
AC AAG47088;
XX
XX 18-OCT-2000 (first entry)
XX
XX Arabidopsis thaliana protein fragment SEQ ID NO: 59312.
DE
XX Protein identification; signal transduction pathway; metabolic pathway;
KW hybridisation assay; genetic mapping; gene expression control; promoter;
KW termination sequence.
XX
XX Arabidopsis thaliana.
OS
XX
XX
XX EP1033405-A2.
XX
PD 06-SEP-2000.
XX
XX 25-FEB-2000; 2000BP-0301439.
XX
XX 25-FEB-1999; 99US-0121825.
PR 05-MAR-1999; 99US-0123180.
PR 09-MAR-1999; 99US-0123548.
PR 23-MAR-1999; 99US-0125788.
PR 25-MAR-1999; 99US-0126264.
PR 29-MAR-1999; 99US-0126785.
PR 01-APR-1999; 99US-0127462.
PR 06-APR-1999; 99US-0128234.
PR 08-APR-1999; 99US-0128714.
PR 16-APR-1999; 99US-0129845.
PR 19-APR-1999; 99US-0130077.
PR 21-APR-1999; 99US-0130449.
PR 23-APR-1999; 99US-0130510.
PR 28-APR-1999; 99US-0130891.
PR 30-APR-1999; 99US-0131449.
PR 30-APR-1999; 99US-0132048.
PR 30-APR-1999; 99US-0132407.
PR 04-MAY-1999; 99US-0132484.
PR 05-MAY-1999; 99US-0132485.
PR 06-MAY-1999; 99US-0132486.
PR 06-MAY-1999; 99US-0132487.
PR 07-MAY-1999; 99US-0132863.
PR 11-MAY-1999; 99US-0134256.
PR 14-MAY-1999; 99US-0134218.
PR 14-MAY-1999; 99US-0134219.
PR 14-MAY-1999; 99US-0134221.
PR 14-MAY-1999; 99US-0134370.
PR 18-MAY-1999; 99US-0134768.
PR 19-MAY-1999; 99US-0134941.
PR 20-MAY-1999; 99US-0135124.
PR 21-MAY-1999; 99US-0135353.
PR 24-MAY-1999; 99US-0135629.
PR 25-MAY-1999; 99US-0136021.
PR 27-MAY-1999; 99US-0136392.
PR 28-MAY-1999; 99US-0136782.
PR 01-JUN-1999; 99US-0137222.
PR 03-JUN-1999; 99US-0137528.
PR 04-JUN-1999; 99US-0137502.
PR 07-JUN-1999; 99US-0137724.
PR 08-JUN-1999; 99US-0138094.
PR 10-JUN-1999; 99US-0138540.
PR 10-JUN-1999; 99US-0138847.
PR 14-JUN-1999; 99US-0139119.
PR 16-JUN-1999; 99US-0139452.
PR 16-JUN-1999; 99US-0139453.
PR 17-JUN-1999; 99US-0139492.
PR 18-JUN-1999; 99US-0139454.
PR 18-JUN-1999; 99US-0139455.
PR 18-JUN-1999; 99US-0139456.
PR 18-JUN-1999; 99US-0139457.
PR 18-JUN-1999; 99US-0139458.
PR 18-JUN-1999; 99US-0139459.
PR 18-JUN-1999; 99US-0139460.
PR 18-JUN-1999; 99US-0139461.
PR 18-JUN-1999; 99US-0139462.
PR 18-JUN-1999; 99US-0139463.
PR 18-JUN-1999; 99US-0139750.
PR 18-JUN-1999; 99US-0139763.
PR 21-JUN-1999; 99US-0139817.
PR 22-JUN-1999; 99US-0139899.
PR 23-JUN-1999; 99US-0140353.
PR 23-JUN-1999; 99US-0140354.
PR 24-JUN-1999; 99US-0140695.
PR 28-JUN-1999; 99US-0140823.
PR 29-JUN-1999; 99US-0140991.
PR 30-JUN-1999; 99US-0141287.
PR 01-JUL-1999; 99US-0141842.
PR 01-JUL-1999; 99US-0142154.
PR 02-JUL-1999; 99US-0142055.
PR 06-JUL-1999; 99US-0142590.
PR 08-JUL-1999; 99US-0142803.
PR 09-JUL-1999; 99US-0142920.
PR 12-JUL-1999; 99US-0142977.
PR 13-JUL-1999; 99US-0143542.
PR 14-JUL-1999; 99US-0143624.
PR 15-JUL-1999; 99US-0144005.
PR 16-JUL-1999; 99US-0144085.
PR 16-JUL-1999; 99US-0144086.
PR 19-JUL-1999; 99US-0144325.
PR 19-JUL-1999; 99US-0144331.
PR 19-JUL-1999; 99US-0144332.
PR 19-JUL-1999; 99US-0144333.
PR 19-JUL-1999; 99US-0144334.
PR 19-JUL-1999; 99US-0144335.
PR 20-JUL-1999; 99US-0144352.
PR 20-JUL-1999; 99US-0144632.
PR 21-JUL-1999; 99US-0144884.
PR 21-JUL-1999; 99US-0144814.
PR 21-JUL-1999; 99US-0145086.
PR 21-JUL-1999; 99US-0145088.
PR 22-JUL-1999; 99US-0145085.
PR 22-JUL-1999; 99US-0145087.
PR 22-JUL-1999; 99US-0145089.
PR 22-JUL-1999; 99US-0145192.
PR 23-JUL-1999; 99US-0145145.
PR 23-JUL-1999; 99US-0145218.
PR 23-JUL-1999; 99US-0145224.
PR 26-JUL-1999; 99US-0145276.
PR 27-JUL-1999; 99US-0145913.
PR 27-JUL-1999; 99US-0145918.
PR 27-JUL-1999; 99US-0145919.
PR 28-JUL-1999; 99US-0145951.
PR 02-AUG-1999; 99US-0146386.
PR 02-AUG-1999; 99US-0146388.
PR 02-AUG-1999; 99US-0146389.
PR 03-AUG-1999; 99US-0147038.
PR 04-AUG-1999; 99US-0147204.
PR 04-AUG-1999; 99US-0147302.
PR 05-AUG-1999; 99US-0147192.
PR 05-AUG-1999; 99US-0147260.
PR 06-AUG-1999; 99US-0147303.
PR 06-AUG-1999; 99US-0147416.
PR 09-AUG-1999; 99US-0147493.
PR 09-AUG-1999; 99US-0147935.
PR 10-AUG-1999; 99US-0148171.
PR 11-AUG-1999; 99US-0148319.
PR 12-AUG-1999; 99US-0148341.
PR 13-AUG-1999; 99US-0148565.

variant of the above mentioned polypeptide sequence. Expression levels of the nucleic acid can be modified to improve the vasculature in transgenic plants and enhance the agronomic properties of such plants. Also the WOL promoter is used to drive expression of a heterologous coding sequence of trees to improve wood production. The WOL nucleic acid may be used as a molecular marker for a qualitative trait loci, e.g., longer roots or enhanced wood production, in molecular breeding of crop plants. The nucleic acid is also useful in DNA amplification assays to identify the endogenous WOL genes, WOL mutant alleles and/or WOL expression products in cultivars as compared to wild-type plants. They can also be used as markers for linkage analysis of qualitative trait loci. The WOL protein and/or antibodies can be used as diagnostic reagents in immunoassays to detect expression of the WOL gene in cultivars and wild-type plants. The WOL protein, its encoding nucleic acid, and its corresponding antibody are useful for improving agronomically valuable plants e.g., trees. This sequence represents a protein relating to the wooden leg (WOL) protein of the invention.

5Q Sequence 1057 AA;

Query Match 48.0%; Score 2475.5; DB 23; Length 1057;
Best Local Similarity 50.8%; Pred. No. 1.5e-204;
Matches 535; Conservative 156; Mismatches 251; Indels 111; Gaps 18;

QY 21 MTLKKNNKMMFNNKISSGLKIPSPS-----YQFLGSVKFN----- 57
Db 43 LNSSEKPKRIDFWR-----SGLM--GFARMQOQOQLQHSVAVKMNNNNNNDLGMKKGSTF 96
QY 58 ----KAWKRLVNVVFWVLVSTWTFYSSQAMEKESKTLASMKCDERARMLODFNYS 113
Db 97 IOEHRLLPKALILIIIVGFISSGIYQWMDANKIRREVLVSMCDQARMLODFNYS 156
QY 114 MNHVQAMSLISTPHHGKIPSAIDQRTFSEYDTRTSFERELTSGVAYAMRVLSHREEFE 173
Db 157 VNVHVALAILVSTHYHKNPSAIDQRTFAEYRTAFERPLLSGVAEAKVNVFEREMFE 216
QY 174 RQGWTRKMYSLQNPHKDDYDLALEPSVQEEYAPVIFAQDTVSHVVSVDLMDLSCGE 233
Db 217 RQHNWVTKM-----DRGEPSPVDEYAPVIFQDSVSYLESIDMMSGEE 261
QY 234 DRENVLARSKGKVLTAFFPLIKTNRLGVILTFAVKRDLPSNATPKERIEATNGYLG 293
Db 262 DRENILRARETGKAVLSPFALLETHLGVLTTPVYKSSLPENPTVBERIAATAGYLG 321
QY 294 VDIIESLVNLLQASKQTLNVYDITNHSQIPSMYGT-NVSAD-GLERSVSLFGDP 351
Db 322 AFDVESLVNLLGQAGNQAIVHVDITNASDPLVMYGNQDEEADRSLSHESKLDGDP 381
QY 352 LRKHEMRCPKQPPVPLSMVTGFGILVIALVAHIIHATVSRHKEVEDCDKMKOLKK 411
Db 382 FRKHMKICRYHQKAPIPANVLTVPFLFAIGLVYLYGNAMHIVKVEDDFHEMQLKV 441
QY 412 KAAADVAKSQFLATVSHIEITPMNVLGMLHMLMDTDLVTOQDYVVRTAQAGKALVSL 471
Db 442 RAAADVAKSQFLATVSHIEITPMNVLGMLHMLMDTDLVTOQDYVVRTAQAGKALIAL 501
QY 472 INEVLDOAKISGKLEFEVDFLGLDVLISFSSKQKQGVELAVYISDRVPMGLIG 531
Db 502 INEVLDOAKISGKLEFEVDFLGLDVLISFSSKQKQGVELAVYISDRVPMGLIG 561
QY 532 DPGRFQRLITLMGNSIKFTKGHIFVTVHVLVDELFSIDGETA-----SS 577
Db 562 DSGRFQRLITLMGNSIKFTKGHIFVTVHVLVDELFSIDGETA-----SS 621
QY 578 PESTLUGLPLVADQRQSWNFASFNSGH--RSFEPSPDINLIVSVEDTGVGIPVEAQSR 635
Db 622 SYNTLSGVEAADGRNSWSFKHLVSEEQSLSEFDS--SNRLMVSIEDTGTGIPVLAQGR 680
QY 636 IFTPMQVQPSISRTHGCTGIGLSKCLVGMKEICFSTPKVSGTFTTAVFS----- 691
Db 681 VPMFPQADSSRSNYGGTIGLSKCLVGMKEICFSTPKVSGTFTTAVFS----- 740
QY 692 ----NGMOPAKRKNDNNQPIFSEFRGMKAVVVDHPRAPAKVSWYHFQRLGRVVEVPRVE 747

Db 741 CSAINH-----KKPNVHLPSTPKGKKAIVVDKAPVRAAVTRYHMKRLGINVDVTSLK 795
QY 748 QAL-----HYLKIGT-----TTVMILIEQIWM--NRADDFIKKLOK-----DPLFLSPKL 792
Db 796 TAVVAAAFENGSPGPTKQLODMILVEKDSWISTEDSEIRLLNSRTNGNVHHSKPKL 855
QY 793 ILLANSVSEISALCTGIDPPIVIVKPLRSMALATLQRLGIGIGIREPPQHKGPALIL 852
Db 856 ALFATNITNSFDRKASGADTVIMKPLRSMIGACLQOVLELTKTROQHPGSSPATL 915
QY 853 RNLLGRKILVDDNNVNLVRAAGALKYGVADVCABSGIKALISLLKPPHEPACPMDIQ 912
Db 916 KSLLTGKKILVDDNNVNLVRAAGALKYGVADVCABSGIKALISLLKPPHEPACPMDIQ 975
QY 913 MPENDGFATRIIRDMSEEMMKRIKNGEALIVNGNKTSWHLPLVMTADVIOATHEECL 972
Db 976 MPQWDGFATRIIRDMSEEMMKRIKNGEALIVNGNKTSWHLPLVMTADVIOATHEECL 1023
QY 973 KCGMDGVYVKPFEABQLYREVSRFFN-----SPS 1001
Db 1024 KSGMDGVYVKPFEABQLYREVSRFFN-----SPS 1056
RESULT 14
ID AA022570 standard; Protein; 1057 AA.
XX AA022570;
XX 28-OCT-2002 (first entry)
XX Wooden leg (WOL) gene related protein SEQ ID No 24.
XX Wooden leg; WOL; vasculature; transgenic plant; agronomic; longer root;
XX wood production; plant; promoter; tree; crop plant.
XX Arabidopsis thaliana.
XX WO200244337-A2.
XX 06-JUN-2002.
XX 29-NOV-2001; 2001WO-US45053.
XX 29-NOV-2000; 2000US-253739P.
XX (UTNY) UNIV NEW YORK STATE.
XX (HELA) HELARIUTTA Y.
XX (MAHO) MAHONEN A P.
XX (BONK) BONKE A W M.
XX (KAUP) KAUPPINEN L.
XX (RIIK) RIIKONEN M.
XX Helariutta Y, Mahonen AP, Bonke AMW, Kauppinen L, Riikonen M;
XX Benfey PN;
XX WPI; 2002-599423/64.
XX Novel isolated polypeptide (WOODEN LEG) with ability to regulate a set
XX of asymmetric cell divisions that establish vascular tissue in root and
XX hypocotyl development, useful for improving agronomically valuable
XX plants -
XX Disclosure; Page 167-171; 187pp; English.
XX The invention relates to an isolated WOODEN LEG (WOL) polypeptide,
XX comprising 15 contiguous amino acids of a fully defined Arabidopsis
XX WOODEN LEG protein sequence of 1057 amino acids as given in the
XX specification, and to its encoding nucleic acid. The invention also
XX relates to an amino acid sequence of domains of protein, e.g., N-terminal
XX region, C-terminal domain, etc; or is a naturally occurring allelic
XX variant of the above mentioned polypeptide sequence. Expression levels of

CC the nucleic acid can be modified to improve the vasculature in transgenic
CC plants and enhance the agronomic properties of such plants. Also the WOL
CC promoter is used to drive expression of a heterologous coding sequence of
CC trees to improve wood production. The WOL nucleic acid may be used as a
CC molecular marker for a qualitative trait loci, e.g., longer roots or
CC enhanced wood production, in molecular breeding of crop plants. The
CC nucleic acid is also useful in DNA amplification assays to identify the
CC endogenous WOL genes. WOL mutant alleles and/or WOL expression products
CC in cultivars as compared to wild-type plants. They can also be used as
CC markers for linkage analysis of qualitative trait loci. The WOL protein
CC and/or antibodies can be used as diagnostic reagents in immunoassays to
CC detect expression of the WOL gene in cultivars and wild-type plants. The
CC WOL protein, its encoding nucleic acid, and its corresponding antibody
CC are useful for improving agronomically valuable plants e.g., trees. This
CC sequence represents a protein relating to the wooden leg (WOL) protein of
CC the invention.

XX Sequence 1057 AA;
Query Match 48.0%; Score 2475.5; DB 23; Length 1057;
Best Local Similarity 50.8%; Pred. No. 1.5e-204;
Matches 535; Conservative 156; Mismatches 251; Indels 111; Gaps 18;
QY 21 MTLKKKONWFWNKISSGLKIPFS-----VQFLGSKFN----- 57
DB 43 LNSSEKPRKIDFWR---SGLM--GFAKMQQQQQLQHSVAVKRMNNNNNDLGNKKGSTF 96
QY 58 ---KAWWRKLVVWVFWVLVSIWTFWYFSSQAMEKKEKTLASDCDERAMLODQFNVS 113
DB 97 IOEHALLPKALILMIIIVGFISSGIYQWMDANKIRREVLVSCDQEARMLDQFVS 156
QY 114 MNHVQAMSLITFFHGKIPSAIDORTSEYDRTSPERPLTSGVAYAVRVILHSEBEFE 173
DB 157 VNHVALAILVSTFHYHKNPSAIDQETAEYATARTAFERPLISGVAYAEKVVNFERENFE 216
QY 174 RQGWRTIRWYSLEQNPVHKDYDLEALEPSPVQSEYAPVIFAQDTVSHVSLDMLSKKE 233
DB 217 RQHNWVKTW-----DRGEPSPVDEYAPVIFPSQSVLSLESDMMSGEE 261
QY 234 DRENVLARSSGKGLVTPAPFLIKTNRLGVILTFAYKRDLPFSNATPKERIEATNGYLG 293
DB 262 DRENILARETGKAVLTSFRLLETHLGVLTFFPVYKSSLPENPTVEERIAATAGYLG 321
QY 294 VFDISLVNLLQOLASKOTILVNYVDITNHSQPSMYGT-NVSAD-GLERSVPLIFDGP 351
DB 322 AFDVESLVNLLQOLAGNOAIVHYVDITNASDPLVYMGNDQDEADRLSHESKLDGDP 381
QY 352 LRKHEMRCEKQKPPWPLVSMVTSFGILVIALVAHIHATVSRILHKVEEDCDKMKOLK 411
DB 382 FRKHMI CHYHQAPLPLNLTVPFLFAIGLVGYLYGAAMHIVKVEDDFHEMQELKV 441
QY 412 KAAADVAKSQFLATVSHSHEIRTPMNGVLGMHMLMDTDLDTQDYVTRTAQASGKALVSL 471
DB 442 RAAADVAKSQFLATVSHSHEIRTPMNGVLGMHMLMDTDLDTQDYVTRTAQASGKALVSL 501
QY 472 INEVLDOAKTESKLEVRDLGLDVLSSSKSQKGVYLAVIDSRVDPDMLIG 531
DB 502 INEVLDRAKIEAGKLESEVPDIDRILDDVLSSLSFSESRNKSILHAFVSDKVEPVK 561
QY 532 DPCRFRQILTNLMGNSIKTEKHIFVTYVHLVDLSEIDGETA-----SS 577
DB 562 DSGRFRQIILNVGNSVKTKEGHIFVKVHLAEQSKDESPKALNGGVSEBIMVVSQ 621
QY 578 PESTLGLPVADQRWENKAFSSNGH--RFEFSPDPINILVSVEDTGVGIPVEAQR 635
DB 622 SYNTLSGYAADRNSWDSFKHLVSEBQSLSEFSDIS-SNVRMLVSIETDGTGIPVLAQR 680
QY 636 IETPMQVGPISIRTEGGFGIGLISKCLVGLMKGRIGFSSPKVGSFTFTFAVES--- 691
DB 681 VFMPFQADSSTSRNTGGTIGLUSISKCLVLMRGQINFISPHIGSTFWFAVLKCDK 740
QY 692 ---NGMQFAERKNDNNQPIFSEFRGMKAVVVDHFRPARAKVSWYHFQRLGIRVEVVRVE 747

DB 741 CSAINHM-----KKNVHEHLPSTFTGKMAIVVDKAPVRAAVTRYHMKRLGINVDVVTSLK 795
QY 748 QAL----HYLKIGT-----TTWNMILIQEIW--NREADDRIKKLOK---DPLFLSPKL 792
DB 796 TAVVAAAFAFERNGSPLPFTKQDMLILVEKDSWISTEDNDSEIRLNSRTNGNVHHSKPL 855
QY 793 ILLANSVSSISEALCTGIDPPIVIVKPLRASMLAATLQRLGIGIRPPOKHGPPALIL 852
DB 856 ALFATNITNSEFDRAKSAGFADTVIMKPLRASMIGACIQVLELRKTRQOHPEGSSPATL 915
QY 853 RULLGRKLLIYDDNNVNI RVAAGALKKGVADVCARSIGIKALISLLKPHHFDACFMDIO 912
DB 916 KSLTUTGKKLLVDDNINVRVRAAGALKKPGAEVCAESQVAGLGLQIPHFTFDACFMDIO 975
QY 913 MPMDGFEATRRIRIOMEEMNKRIKNGEALIVENGKTSWHLPLVLTAMTADTVQATHEECL 972
DB 976 MPQMDGFEATRRIRIOMEEMNKRIKNGEALIVENGKTSWHLPLVLTAMTADTVQATHEECL 1023
QY 973 KQMDGYVSKPEAEOLYREVSFFN-----SPS 1001
DB 1024 KSGMDGYVSKPEAEOLYREVSFFN-----SPS 1056
RESULT 15
AAE33694
ID AAE33694 standard; Protein; 1057 AA.
XX
AC AAE33694;
XX
DT 16-APR-2003 (first entry)
XX
DE Arabidopsis thaliana histidine kinase 4 (AHK4)-WOL, CRE1 protein.
XX
KW Shoot formation; senescence; transgenic; transgenic plant; agriculture;
KW cell proliferation; shoot meristem formation; leaf development; AHK;
KW photosynthesis; histidine kinase; enzyme; CRE1.
XX
OS Chimeric - Arabidopsis thaliana.
OS Chimeric - Unidentified.
XX
XX WO200299079-A2.
XX
PD 12-DEC-2002.
XX
XX 06-JUN-2002; 2002WO-US18066.
XX
XX 06-JUN-2001; 2001US-296554P.
XX
XX (GEO) GEN HOSPITAL CORP.
XX
XX Sheen J, Hwang I;
XX
XX WPI; 2003-140613/13.
XX
XX Increasing yield in plant, increasing shoot formation in a plant, or
XX delaying senescence in a plant such as wheat, rice, maize, barley,
XX potato, by using transgenes that regulate cytokinin response
XX
XX Disclosure; Page 80-82; 87pp; English.
XX
XX The present invention relates to a novel method of increasing yield in a
XX plant, increasing shoot formation or delaying senescence in a plant. The
XX method involves introducing into plant cells, a transgene having a B-type
XX response regulator operably linked to a promoter functional in plant
XX cells to yield transformed plant cells or whose expression reduces the
XX expression of A-type response regulator in the cells of the plant and
XX regenerating a plant from the transformed cells. The method is useful
XX for increasing the yield in a plant, increasing the shoot formation or
XX delaying senescence in a plant such as wheat, rice, maize, barley,
XX potato, tomato, soybean, tomato, oat, cotton and sunflower. The method
XX is useful for variety of agricultural and commercial purposes including
XX improving and enhancing photosynthesis, promoting cell proliferation,
XX shoot meristem formation, promoting leaf development, increasing crop

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OM protein - protein search, using sw model

Run on: November 28, 2003, 14:02:30 ; Search time 27.0799 Seconds
(without alignment)
6681.678 Million cell updates/sec

Title: US-09-918-508-2_COPY_196_1176

Perfect score: 5019

Sequence: 1 KARGERKEKHVQLAPK.....SKPPEEVLYTAVARFFPEFC 981

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 673684 seqs, 18443283 residues

Total number of hits satisfying chosen parameters: 673684

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications AA.*

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- 2: /cgn2_6/ptodata/2/pubpaa/PCT_NEW_PUB.pep.*
- 3: /cgn2_6/ptodata/2/pubpaa/US06_NEW_PUB.pep.*
- 4: /cgn2_6/ptodata/2/pubpaa/US06_PUBCOMB.pep.*
- 5: /cgn2_6/ptodata/2/pubpaa/US07_NEW_PUB.pep.*
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- 7: /cgn2_6/ptodata/2/pubpaa/US08_NEW_PUB.pep.*
- 8: /cgn2_6/ptodata/2/pubpaa/US08_PUBCOMB.pep.*
- 9: /cgn2_6/ptodata/2/pubpaa/US09A_PUBCOMB.pep.*
- 10: /cgn2_6/ptodata/2/pubpaa/US09B_PUBCOMB.pep.*
- 11: /cgn2_6/ptodata/2/pubpaa/US09C_PUBCOMB.pep.*
- 12: /cgn2_6/ptodata/2/pubpaa/US09_NEW_PUB.pep.*
- 13: /cgn2_6/ptodata/2/pubpaa/US10A_PUBCOMB.pep.*
- 14: /cgn2_6/ptodata/2/pubpaa/US10B_PUBCOMB.pep.*
- 15: /cgn2_6/ptodata/2/pubpaa/US10C_PUBCOMB.pep.*
- 16: /cgn2_6/ptodata/2/pubpaa/US10_NEW_PUB.pep.*
- 17: /cgn2_6/ptodata/2/pubpaa/US60_NEW_PUB.pep.*
- 18: /cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	5019	100.0	1176	10	US-09-918-508-2
2	4991.5	99.5	1173	14	US-10-135-322-19
3	3291.5	65.6	1270	15	US-10-101-464A-979
4	2973.5	59.2	890	15	US-10-101-464A-958
5	2764	55.1	1002	15	US-10-101-464A-957
6	2685.5	53.5	1036	10	US-09-918-508-4
7	2651.5	52.8	1044	15	US-10-101-464A-956
8	2604	51.9	997	15	US-10-101-464A-977
9	2595.5	51.7	1092	14	US-10-135-322-18
10	2545.5	50.7	1057	10	US-09-918-508-6
11	2539.5	50.6	1057	14	US-10-135-322-5
12	2539.5	50.6	1057	14	US-10-135-322-24
13	2363	47.1	974	15	US-10-126-120-2
14	1378	27.5	480	15	US-10-101-464A-978
15	1132.5	22.6	426	15	US-10-101-464A-124

16	1063.5	21.2	482	15	US-10-101-464A-955
17	1010.5	20.1	412	15	US-10-101-464A-905
18	860	17.1	274	14	US-10-135-322-8
19	844	16.8	289	14	US-10-135-322-10
20	688	13.7	1081	10	US-09-424-951-4
21	642.5	12.8	2150	14	US-10-135-322-17
22	594.5	11.8	1018	15	US-10-101-464A-909
23	572.5	11.4	1829	15	US-10-156-761-10049
24	563.5	11.2	971	14	US-10-116-048-2
25	563.5	11.2	2471	14	US-10-116-048-4
26	549.5	10.9	1240	15	US-10-101-464A-376
27	546	10.9	1447	15	US-10-156-761-8624
28	522	10.4	816	15	US-10-101-464A-827
29	514	10.2	747	12	US-10-100-294A-27
30	513.5	10.2	418	10	US-09-424-951-2
31	487	9.7	1220	15	US-09-801-368-332
32	478	9.5	1383	15	US-10-156-761-13096
33	462	9.2	185	15	US-10-101-464A-822
34	455	9.1	123	14	US-10-135-322-12
35	451.5	9.0	1373	12	US-10-032-585-7129
36	435.5	8.7	738	12	US-10-171-404A-36
37	430.5	8.6	170	15	US-10-101-464A-116
38	426	8.5	129	15	US-10-101-464A-828
39	426	8.5	496	15	US-10-101-464A-906
40	421.5	8.4	717	12	US-10-171-404A-38
41	414	8.2	100	14	US-10-135-322-29
42	390	7.8	206	15	US-10-101-464A-120
43	380.5	7.6	264	14	US-10-101-464A-959
44	360.5	7.2	104	14	US-10-135-322-30
45	357.5	7.1	773	12	US-10-171-404A-34

ALIGNMENTS

RESULT 1

US-09-918-508-2 Application US/09918508
; Sequence 2, Application US/09918508
; Patent No. US20020177162A1
; GENERAL INFORMATION:
; APPLICANT: KAKIMOTO, TATSUO
; APPLICANT: HIGUCHI, MASAYUKI
; APPLICANT: INOUE, TSUTOMU
; TITLE OF INVENTION: ANALYSIS OF AGONIST-ACTIVITY AND ANTAGONIST-ACTIVITY
; FILE REFERENCE: Q65478
; CURRENT FILING DATE: 2001-08-01
; PRIOR FILING DATE: 2001-03-15
; PRIOR FILING DATE: 2001-03-15
; NUMBER OF SEQ ID NOS: 22
; SOFTWARE: Patent in Ver. 2.1
; SEQ ID NO 2
; LENGTH: 1176
; TYPE: PRT
; ORGANISM: Arabidopsis thaliana
US-09-918-508-2

Query Match	100.0%	Score	5019	DB	10	Length	1176
Best Local Similarity	100.0%	Pred. No.	0				
Matches	981	Conservative	0	Mismatches	0	Indels	0
						Gaps	0
Qy	1	KARGERKEKHVQLAPK	QQAQTSRSGAGRWKRNILLGILGVGSFVWFWDTNE	60			
Db	196	KARGERKEKHVQLAPK	QQAQTSRSGAGRWKRNILLGILGVGSFVWFWDTNE	255			
Qy	61	EIMKRETLANMCDERARV	LQDFNVSLNHVALSLVSTFHGKIPSAIDORTPEEY	120			
Db	256	EIMKRETLANMCDERARV	LQDFNVSLNHVALSLVSTFHGKIPSAIDORTPEEY	315			
Qy	121	ERTNFERPLTSGVAYALKV	PHSREKPEKEGHGWAIKQMETEDQTVVQDCVPENFDPAP	180			
Db	316	ERTNFERPLTSGVAYALKV	PHSREKPEKEGHGWAIKQMETEDQTVVQDCVPENFDPAP	375			

QY 181 DEYAPVIFAQTVSHIVSDMMSCBEDRENILRARASGKGLVLTSPFKLLKSNHGLVLT 240
Db 376 DEYAPVIFAQTVSHIVSDMMSCBEDRENILRARASGKGLVLTSPFKLLKSNHGLVLT 435
QY 241 AVYDTSPPDQTEQORVEATIGYLGASVDMPSLVEKLLHQLASKQTIADVDTNTSGL 300
Db 436 AVYDTSPPDQTEQORVEATIGYLGASVDMPSLVEKLLHQLASKQTIADVDTNTSGL 495
QY 301 IKMYGSEIGDISEQHISSLDGDPSPRNHEHCRPKHLPIPTWTAITPSILVITFLVGY 360
Db 496 IKMYGSEIGDISEQHISSLDGDPSPRNHEHCRPKHLPIPTWTAITPSILVITFLVGY 555
QY 361 ILYEAINRIATVEEDCQKRELKARAAADIAKSOFLATVSHETPTMNGVGLMKMLMD 420
Db 556 ILYEAINRIATVEEDCQKRELKARAAADIAKSOFLATVSHETPTMNGVGLMKMLMD 615
QY 421 TDLDAKQMDYAQTAHSGSKDITSLINEVLDQAKIESGRLELENVPPFMDRFLDNVSSLS 480
Db 616 TDLDAKQMDYAQTAHSGSKDITSLINEVLDQAKIESGRLELENVPPFMDRFLDNVSSLS 675
QY 481 GKANEKGIELAVYSSQVDPVVDGDPSPRFRQIITNLVGNISIKFTQERGHIFISVHLADEV 540
Db 676 GKANEKGIELAVYSSQVDPVVDGDPSPRFRQIITNLVGNISIKFTQERGHIFISVHLADEV 735
QY 541 KEPLTIEDAVLKQRLALGCSSEGETVSGFPVAVNAGSWKNFKTCYSTESQNSDQIKLLVT 600
Db 736 KEPLTIEDAVLKQRLALGCSSEGETVSGFPVAVNAGSWKNFKTCYSTESQNSDQIKLLVT 795
QY 601 VEDTGVIPIVDAQGRIFTPFMQADSSRTYGGTIGLSISKRLVELMQEMGFVSPGI 660
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QY 661 GSTSFSGVFGKAEINTSITKLERFDLAIQFTGLRALVIDNRNIRAEVTRVYELRRLGIS 720
Db 856 GSTSFSGVFGKAEINTSITKLERFDLAIQFTGLRALVIDNRNIRAEVTRVYELRRLGIS 915
QY 721 ADVSSLRMACTCCISKLENAMILIDKAWNKEEFSVLDDELFTSRKVTFTVRPKIFLLA 780
Db 916 ADVSSLRMACTCCISKLENAMILIDKAWNKEEFSVLDDELFTSRKVTFTVRPKIFLLA 975
QY 781 TSATLTERSEMKSTGLIDEVVIKPLRMSVLICQIETLVNGKKQPNQRNRLGHLREK 840
Db 976 TSATLTERSEMKSTGLIDEVVIKPLRMSVLICQIETLVNGKKQPNQRNRLGHLREK 1035
QY 841 QILVDDNLVNRVVAEGALKKYGAIIVTCVSGKAAALAMLPKPPHNFDAFMDLQMPMDGF 900
Db 1036 QILVDDNLVNRVVAEGALKKYGAIIVTCVSGKAAALAMLPKPPHNFDAFMDLQMPMDGF 1095
QY 901 EATRVRLEBREINKKIASGEVSAPMFCKFSMSHVPILAMTADVIQATHECMKCGMDGY 960
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Db 1156 VSKPPEEVLATAVARPEPC 1176

RESULT 2

US-10-135-322-19
; Sequence 19, Application US/10135322
; Publication No. US20020173017A1
; GENERAL INFORMATION:
; APPLICANT: BENFEY, PN
; APPLICANT: HELARIUTTA, Y
; APPLICANT: MAHONEN, AP
; APPLICANT: MAHONEN, AP
; APPLICANT: BOWKE, AWM
; APPLICANT: KAUPPINEN, L
; APPLICANT: RIIKONEN, M
; TITLE OF INVENTION: "WOODEN LRG-GENE, PROMOTER AND USES THEREOF"
; FILE REFERENCE: 5914-086-999
; CURRENT APPLICATION NUMBER: US/10/135,322
; CURRENT FILING DATE: 2002-04-30

; PRIOR APPLICATION NUMBER: 60/253,739
; PRIOR FILING DATE: 2000-11-29
; NUMBER OF SEQ ID NOS: 43
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 19
; LENGTH: 1173
; TYPE: PRT
; ORGANISM: Arabidopsis thaliana
US-10-135-322-19

Query Match 99.5%; Score 4991.5; DB 14; Length 1173;
Best Local Similarity 99.7%; Pred. No. 0;
Matches 978; Conservative 0; Mismatches 0; Indels 3; Gaps 1;

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Db 196 KARGERKVKHLOEALAPKKQOQRAQTSRGAGRWKKNILLGILGGVSFVSWFWMDTNE 255
QY 61 EIIMKRRETLANMCDERARVLQDQPNVSLNHVHALSILVSTFHHGKIPSAIDQRTFEYT 120
Db 256 EIIMKRRETLANMCDERARVLQDQPNVSLNHVHALSILVSTFHHGKIPSAIDQRTFEYT 315
QY 121 ERTNERELTSGVAVALKVPHSERKFEKEHGWAIKKMETEDQTVQOCVPENFDPAIQ 180
Db 316 ERTNERELTSGVAVALKVPHSERKFEKEHGWAIKKMETEDQTVQOCVPENFDPAIQ 375
QY 181 DEYAPVIFAQTVSHIVSDMMSCBEDRENILRARASGKGLVLTSPFKLLKSNHGLVLT 240
Db 376 DEYAPVIFAQTVSHIVSDMMSCBEDRENILRARASGKGLVLTSPFKLLKSNHGLVLT 435
QY 241 AVYDTSPPDQTEQORVEATIGYLGASVDMPSLVEKLLHQLASKQTIADVDTNTSGL 300
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QY 301 IKMYGSEIGDISEQHISSLDGDPSPRNHEHCRPKHLPIPTWTAITPSILVITFLVGY 360
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QY 361 ILYEAINRIATVEEDCQKRELKARAAADIAKSOFLATVSHETPTMNGVGLMKMLMD 420
Db 556 ILYEAINRIATVEEDCQKRELKARAAADIAKSOFLATVSHETPTMNGVGLMKMLMD 615
QY 421 TDLDAKQMDYAQTAHSGSKDITSLINEVLDQAKIESGRLELENVPPFMDRFLDNVSSLS 480
Db 616 TDLDAKQMDYAQTAHSGSKDITSLINEVLDQAKIESGRLELENVPPFMDRFLDNVSSLS 675
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QY 228 LKSNHGLVLTFAVYDTSPPDATERQORVEATGYLGASVDMPSLVEKLHLQALASKQTI 287
Db 124 LKSNHGLVLTFAVYDTSPPDATERQORVEATGYLGASVDMPSLVEKLHLQALASKQTI 183
QY 288 AVDYDVTNTSGLIKMYGSEIGDISEQHISLSDPGDPSRNHEHCHREKPKLPIPTWATIP 347
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QY 348 SILVLVITFLVGYLYXBAINRIATVEDDCOKRELKARAEAAADIAKSOFLATVSHERTP 407
Db 244 SVGLLVITLVGHIFAHAINRIKVEEDYQMWELKARAEAAADIAKSOFLATVSHERTP 303
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Db 304 MGVGLGMLKMLDITDLDKQMDVTAQTAHAGSGKDLTSLINEVLDQAKIESGRLELVNPPFD 363
QY 468 MRFLDNVSLLSKANEGIELAVYSSOVDPVVGDPSPRFRQLITNLVGNISIKTQER 527
Db 364 LRLALDNVLSLGRSNEKIELAVYSSOVDPVVGDPSPRFRQLITNLVGNISIKTQER 422
QY 528 GHIFISVHLADEVKEPLTIEDAVLKORLALGCSSE-----SGETVSGFPANWAGSMKNPK 582
Db 423 GHIFVSVHLLSEGCQHDPRD--VEKLSNLVEDTSDKTFNTLSGFQVVDKRSNERFK 480
QY 583 TCYSTESQSDQI-----KLVTVEDTVGIPVDAQGRIFTPFMQADSTSTRTYGGTI 636
Db 481 -----KLNRSDDQDVNESVEVLTVEDTVGVIAREAQSRIFTPFMQADSTSTRTYGGTI 535
QY 637 GLSISRLVELMGEVSEPGIGSTFTFTGFGKAEWTSTIKLERDLAIQERTGLR 696
Db 536 GLSISKCLVDLMHGEVSEPGTGTFTFTFPFAKCEMNCLEVKQNDYSIIEPRGLR 595
QY 697 ALVIDNRNRAEYRYELERLIGISADIVSSLRMACTCCIS-----KLENLAMILIDKDAW 751
Db 596 ALVIDKRRHRAEYRYELERLISVDVACSLKACTYLSNPSRELSDPMDVLDKDAW 655
QY 752 NKE-----RPSVLDELFTASKVTTFTTRVPKIFILATISATITERSEMKSTGLIDEVILKPLR 806
Db 656 DRQGTGLMNLISLWKHRQNSGVISIR-PKIFILATISATITERSEMKSTGLIDEVILKPLR 714
QY 807 MSVLICCLQETLVNGKKRQPNROR-RNLGHLRLKQILVVDONLNNRVAEGALKKYGAI 865
Db 715 LSVLISFLQELONGKKRSDRRKSVTLGSLKGRILVVDONLNNRVAEGALKKYGAI 774
QY 866 VTCVSGKAALAMLPKPPHNFDA CFMDLQMPEDMGFEATRRVRELEREINKKIASGEVSAE 925
Db 775 VTCVSGKDAVAKLPQPHDFACFMDLQMPEDMGFEATRRVRELEREINKKIASGEVSD 834
QY 926 MECKSSWVPIAMTADVIQATHECMKCGMDGVYKPFEBEVLVAVARFFE 979
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RESULT 5

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US-10-101-464A-957
; Sequence 957, Application US/10101464A
; Publication No. US20030046728A1
; GENERAL INFORMATION:
; APPLICANT: Strabala, Timothy
; APPLICANT: Nieuwenhuizen, Nicolaas
; APPLICANT: Higgins, Colleen M.
; TITLE OF INVENTION: Compositions Isolated from Plant Cells
; TITLE OF INVENTION: and Their Use in the Modification of Plant Cell Signaling
; FILE REFERENCE: 11000.1020c2
; CURRENT APPLICATION NUMBER: US/10/101,464A
; CURRENT FILING DATE: 2002-03-18
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; PRIOR APPLICATION NUMBER: 09/704,302
; PRIOR FILING DATE: 2000-11-01
; PRIOR APPLICATION NUMBER: 09/228,986
; PRIOR FILING DATE: 1999-01-12
; PRIOR APPLICATION NUMBER: 60/162,866
; PRIOR FILING DATE: 1999-11-01
; PRIOR APPLICATION NUMBER: PCT/US00/00724
; PRIOR FILING DATE: 2000-01-11
; NUMBER OF SEQ ID NOS: 989
; SOFTWARE: Fast-Seq for Windows Version 4.0
; SEQ ID NO 957
; LENGTH: 1002
; TYPE: PRT
; ORGANISM: Eucalyptus grandis
US-10-101-464A-957

Query Match 55.1%; Score 2764; DB 15; Length 1002;
Best Local Similarity 58.4%; Pred. No. 6,7e-245;
Matches 563; Conservative 140; Mismatches 223; Indels 38; Gaps 12;

QY 35 WRKNVILLGILGGVSFVWFWDTNHEIIMKRETLANCMDEARVQLQDFNVSLNHVHA 94
Db 47 WRK-LLYTVWFCAFMFSLMIFMSQALEKKETLASCMDERAQMLQDFNVSMNHVQA 105
QY 95 LSLVSTFHHGKIPSAIDQRTFEEYTERTNFERPLTSGVAYALKVPHSREKFEKHGWA 154
Db 106 MSILSTFHHGKSPSALDQTTFAEYTKRTAFERPLTSGVAYAVRVLHSEAEFEKQGHWP 165
QY 155 IKKMETEDQTV--QDCVPENFDPAIQDEYAPVIPAQETVSHIVSDMMSCBEDRENIL 212
Db 166 IQMDTLEQNLVHKDDFDEVLPEPIQBEYAPVIPAQETVSHIVSDMMSCBEDRENIL 225
QY 213 RARASCKGVLTSPEKLKSNHGLVLTFAVYDTSPPDATERQORVEATGYLGASVDMPS 272
Db 226 RARASCKGVLTAFFPLIKTNRLGVLITFAVYKTLFNSNATPDERIQATAGYIGFIHQ 285
QY 273 LVEKLLHQLASQTTIADVDTNTSGLIKMYGSEIGDISEQHISLSDPGDPSRNHEHCH 332
Db 286 LVEKLLQLASKQNLVNLVLTNTGSHFISMYGSEADDALEIVSTLNFDPFRKHEMRC 345
QY 333 RPKHKLPIPTWATIPSLVLTFLVGYLYXBAINRIATVEDDCOKRELKARAEAAADIA 392
Db 346 RPKQPPFPWLAITTSYGLFVIAMLTGHCYATVARIKVEDDYQKMWELKQAEAAADIA 405
QY 393 KSQFLATVSHERTPMGVGLGMLKMLDITDLDKQMDVTAQTAHAGSGKDLTSLINEVLD 452
Db 406 KSQFLATVSHERTPMGVGLGMLKMLDITDLDVTOQDYVTRTAQASGKALVSLINEVLD 465
QY 453 KIESGRLELVNPPFDMPRFLDNVSLLSKANEGIELAVYSSOVDPVVGDPSPRFRQI 512
Db 466 KIESGKLEAVQFDLRAILDVLSFGSKQEGVELAVFISDQVPEKLGDPGRFRQI 525
QY 513 ITNLVGNISIKTQERGHIFISVHLADEVKEPLTIEDAVLKORLALGCSSEGTSGFP 572
Db 526 ITNLVGNISIKT-EKGHIFVTVHLAQEVMDSLDVETE-----SSKNLTLSGFPVA 574
QY 573 NAWGSMKNPK-----CYSTESQSDQIQLVTVEDTVGIPVDAQGRIFTPFMQADS 625
Db 575 ERLLSWAKFTFSQHERVC-SYPSSTVDLINLIVSVEDTVGIPFEAQCRVTFPFMQVGP 633
QY 626 STSRTYGGTIGLSISKRELVELMGEVSEPGIGSTFTFTGFGKAEWTSTIKLERF 685
Db 634 SISRTHGCTGIGLSISKRELVELMGEVSEPGIPVNGSTFTFTFVNGHSLNLYTTCQM 693
QY 686 ----DLAIQETGLRALVIDNRNRAEYRYELERLIGISADIVSSLRMACTCCISKLENL 741
Db 694 NNQNSANSEPEGMSALVWDPRSRAKYSKHVQLGQVEIVSDNLQVLSLSKRPRI 753
QY 742 AMILIDKDAWKE-EFVSVL--DEL-FTRSKVTFTTRVPKIFILATISATITERSEMKSTGLI 797
Db 754 DMVLIEBEVNMNDSLSILFVDQLRHIDQKVT----PRLFLAKSISISRSDNVTCDTHS 809
QY 798 DEVVIKPLRMSVLICCLQETLVN----GKKRQPNRQNRNLGHLRLKQILVVDONLNNR 853
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      810 PAVIMKPLRASVAAACLQRTGMNGMKNYRNGEVSRLSLQHLLGRKLIIVDDNKVNLIK 869
      854 VAEGALKKYGCAIVTCVESGKAALAMLEKPPHNFDA CFMDLQMPENDGFEATRRVRELEREI 913
      870 VAAGALKRYGAEVLVCVESGKEAISLLTPPHSFYACFNDIQMPGNDGFEATKTIRDVEKSV 929
      914 NKKIASGEVSAEMFCFSGMWVPIAMTADVIOATHEECWKCGMDGVSKPPEEVLYTA 973
      930 NPKIQIGEVSAEAGHNVLIWHPVPIAMTADVIHATQECMKCGMDGVSKPPEAQLYRE 989
      974 VARF 977
      990 VSRF 993

RESULT 6
US-09-918-508-4
; Sequence 4, Application US/0918508
; Patent No. US20030177162A1
; GENERAL INFORMATION:
; APPLICANT: KAKIMOTO, TATSUO
; APPLICANT: HIGUCHI, MASAYUKI
; APPLICANT: INOUE, TSUTOMU
; TITLE OF INVENTION: ANALYSIS OF AGONIST-ACTIVITY AND ANTAGONIST-ACTIVITY
; TITLE OF INVENTION: TO CYTOKININ RECEPTOR
; FILE REFERENCE: Q65478
; CURRENT APPLICATION NUMBER: US/09/918,508
; CURRENT FILING DATE: 2001-08-01
; PRIOR APPLICATION NUMBER: JP 2001-073812
; PRIOR FILING DATE: 2001-03-15
; NUMBER OF SEQ ID NOS: 22
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 4
; LENGTH: 1036
; TYPE: FRT
; ORGANISM: Arabidopsis thaliana
US-09-918-508-4

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511 KISGKLEBVEFPDLRGILDDVLSSKSKQKGVELAVISORVFDMLIGDPRFRQI 570
513 ITNLVGNISKPTOERGHIFISVHLADRVKBLPTTIEDAVLKQRLALGCSSESGETVSGPPAV 572
571 LTNLMGNSIKFT-EKGHIFVTHLVDELFSIDGETA-----SSPESTLSGLPVA 619
573 NAMGSNKEFKTCYSTESQNS-----DOI KLLVTVEDTGVPIDVDAQGRIFTFPMQADSST 627
620 DQRSWENPK-AFSSNGHRSEFSPDDINLI VSVEDTGVGIPVBAQGRIFTFPMQVGPSSI 678
628 SRTVGGTIGLISIKRVLVLMQGBMGFVSPBGIGSTFSFTGVFG-----KAETNPSI 679
679 SRTHGGTIGLISIKCLVGLMKGBIGFSSTPKVGSTFTTAVFNGMGQPAERKDNNOPI 738
680 TKLERPDLAQFTGLRALVTDNNIRAEVTRYELRLRIGISADTVSSLRMACTCCISKLE 739
739 -----PSEFGMKAVVDHPPAKASVWHYFQRLGIRFEVVPVREQALHVKIGTT 789
740 NLAMILDKOANKBEFSVLDELFTRSKVTFTRVFKIPLIATSLATLTERSEMKSTGLIDE 799
790 TVNNLIQEITWNREADDFIKKL---QKDPFLFSFKILLANSVE-SSISEALCTG-IDP 844
800 --VVIKPLRMSVLTCLOETLVNGKKQPNRQ---RRNLGHLRLREKQILVDDDLNVRV 854
845 PIVIVKPLRASMLAATLQRLGLGIRPPOHKGPPALIRNLLGLRKLIVDDNNVNLRV 904
855 AEGALKYKGAIVTCVSGSKAALAMKPPHPNFDA CFMDLQMPMDMGFATRRVRELERIN 914
905 AAGALKYKGAADVVAESGIKAIISLLKPPHEFDACFMDIQMPMDMGFEATRIRDEEEMN 964
915 KKIASGVSAEFMCFKFSWSHVPIILAMTADVIOATHEECMKCMGQGYYSKPFEEVLYTAV 974
965 KRIKNGEALIVENGKTSWHLPLVLMTADVIOATHEECLCKCMGQGYYSKPFEARQLREV 1024
975 ARFF 978
1025 SFFF 1028

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Db 65 KTH-----PSRNSQAGSKFRKKTWRK-VLWMTIIGWFIISACIFWYMSQAABKRE 117
Qy 69 TLAMCDEARVLQDFNYSLNHVALSILVSTFHEHGKIPSAIDQRTFEETERNFERP 128
Db 118 TLGCMCDEARMLQDFNYSMHVQMSILSTFHEHGKOPSAIDQRTFEETERTAFER 177
Qy 129 LSGVAYALKVPHSREKEFEKEHGAIAKMETEDQTV--QDCVPENFDPAPIQDEYAPV 186
Db 178 LTFSTIAYAVRVLHCDREFEKAQWKIKRMDTVEKTPVHKDNLSESESPSPQBEYAPV 237
Qy 187 IFAQETVSHVSDMMSGEEDRENILARASGKGVLTSPFKLLKSHLGVLTFAVYDTS 246
Db 238 IFAQDTIGHVSDMLSGEDRENILARASGKGVLTAPFLIKTNSLGVLTFAVYNDK 297
Qy 247 LPPDATEORVATIGYLGAASYDMPSLVEKLLHOLASKOTIAVDVDTNTSLIKIMYGS 306
Db 298 LPNATPDREIATDYLGAHIESLVKLLQOLASKONI VNVVDTNWNHPSIMYGS 357
Qy 307 EIGDISEQHSILDFGDPGRNHEMHCPRKHLPWPMTAITPSILVLVITFLVGYLYEAI 366
Db 358 DVSEDLVHVSILNFGDPRKHEMCRKFQKGPWPWLAITTSFGILVIALLVGYIFQATV 417
Qy 367 NRIATVEEDCQKRELKARAEADIAKSQFLATVSHIERTPMNGVLGMLMDTDLDAK 426
Db 418 NRIAKVEDDYHKMELKKAEEADVAKSQFLATVSHIERTPMNGVLGMLMDTDLDET 477
Qy 427 QMDYATARGSGKDLTSLINEVLDOAKIESGRLEENVPDMRFILDNVSSLLSGKANBK 486
Db 478 QODYVTAQESGKALVSLINEVLDOAKIESGRIETAVQDFDRAILDVLSLPSGSKQBK 537
Qy 487 GLEAVYSSQVDDVVVGGPSRFRQIITNLVGNISIKFTQERGHIFISVHLADEVKEPLTI 546
Db 538 RVELAVYISENPEKLGIDGPRFRQIITNLVGNISIKFT-EKGHILVTHVLDEV--MNS 593
Qy 547 EDVAVLKQRLALGCSSEGTVSQFPVAVNGSWKNFKTCYSTE-----SQNSDQIKLIV 599
Db 594 TDAEMB-----SATRSLSGFPVDPRLSLAKFET-ESQGPASPVPSPSNPINLI 645
Qy 600 TVEDTGVPIDVDAQGRIFPFMQADSTSRGTGGTGIGLSISKRLVELMQGEMGFVSEPG 659
Db 646 SVEDTGIGIPPEAQPRVFRVQVGSISRTGGTGIGLSISKRLVGMNGSIGFVSIPO 705
Qy 660 IGSTFTVQVQKAETNTSITKLERF---DLAIQETGLRALVIDNRNIRAEVTRYELR 715
Db 706 VGSTFTTAVFDADACSTSECKGQVQVGGQSGTSEFGMKALVVDTRPVANVSKYHIQ 765
Qy 716 RLGISADIVSSIRMACTCCISKLEN---LAMILDKDANKKEEPSVLDELFP-----TR 765
Db 766 RLGIHVEVVADLQ---CLHTIQSGNCRIDVLEWEIWDKD--SGLSAIFDLKLRDMK 819
Qy 766 SKVTFTVRPKIFLLATSATLTERSEMKSTGLIDEVVIKPLRMSVLICLQETL-----818
Db 820 PRVS---PRLLFSLNSISSRMSGATTATGFFVIMKPLRMSLVASQVRVGVNVRIS 875
Qy 819 -VNGKKRQPNRQRLGHLRLREKQILVDDNLVNRVRAEGALKKYCAIVTCVSESGKAALA 877
Db 876 CSNGE--SPSLFLRN---LLRGKILVDDNKNVLRVABGALKKYGADVCTDSGEKAIA 930
Qy 878 MLKDPHDFDACFMDLQMPMDGFEATRVRVLEIREINKIASGEVSAEMFCFSSWHVPI 937
Db 931 LURPHDFDACFMDIQMPGMDGFEATRIRQEBQTPSPKEFLFGQSSSEPRENISNHLPI 990
Qy 938 LAMTADVIQATHEECMKGMGDKGVSKPFEEVLYTAVARFF 978
Db 991 LAMTADVIQATHEECTYKMDGVSKPFEEAQFLREVSRFF 1031
```

RESULT 8

US-10-101-464A-977

; Sequence 977, Application US/10101464A

; Publication No. US20030046728A1

; GENERAL INFORMATION:

```
; APPLICANT: Strabala, Timothy
; APPLICANT: Nieuwenhuizen, Nicolaas
; APPLICANT: Higgins, Colleen M.
; TITLE OF INVENTION: Compositions Isolated from Plant Cells
; TITLE OF INVENTION: and their Use in the Modification of Plant Cell Signaling
; FILE REFERENCE: 11000.1020c2
; CURRENT APPLICATION NUMBER: US/10/101,464A
; CURRENT FILING DATE: 2002-03-18
; PRIOR FILING DATE: 09/704,302
; PRIOR FILING DATE: 2000-11-01
; PRIOR APPLICATION NUMBER: 09/228,986
; PRIOR FILING DATE: 1999-01-12
; PRIOR APPLICATION NUMBER: 60/162,866
; PRIOR FILING DATE: 1999-11-01
; PRIOR APPLICATION NUMBER: PCT/US00/00724
; PRIOR FILING DATE: 2000-01-11
; NUMBER OF SEQ ID NOS: 989
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 977
; LENGTH: 977
; TYPE: PRT
; ORGANISM: Eucalyptus grandis
; US-10-101-464A-977
```

Query Match 51.9%; Score 2604; DB 15; Length 977;

Best Local Similarity 54.1%; Pred. No. 3.6e-230;

Matches 547; Conservative 149; Mismatches 240; Indels 76; Gaps 15;

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Qy 10 VHLQALAPKQQQAQTSRSGAGWRKXNILLGLGVSPVWVWFWTNEIIMKRETT 69
Db 14 VKLNEQVGTK----RGYTFIQSNRAWIPKILVSVGMAFLSMSTYRRWDADIKVRREV 69
Qy 70 LANMCDERARVLQDFNYSLNHVALSILVSTFHEHGKIPSAIDQRTFEETERNFERP 129
Db 70 LVSMCDQARMLKQDFSVSNVHVALILVSTFHYKNPASIDQRTFAETARTAFERPL 129
Qy 130 TSGVAYALKVPHSREKEFEKEHGAIAKMETEDQTVQDCVPENFDPAPIQDEYAPVIPA 189
Db 130 LSGVAYAEVNTSEKEFEQHGHTIKTEKQ-----PSPVRDEYAPVIFS 175
Qy 190 QETVSHIVSDMMSGEEDRENILARASGKGVLTSPFKLLKSHLGVLTFAVYDTSIPP 249
Db 176 QETVSYIESLDMMSGEEDRENILARATGKAVLTSPFLLGSHLGVLTTPPVYKSKLPP 235
Qy 250 DATEORVATIGYLGAASYDMPSLVEKLLHOLASKOTIAVDVDTNTSLIKIMYGSIG 309
Db 236 NPTVEERIEAVGYLGAFDVESLVENLLGQDQNALVNVYDVNTSSESLIMYGHQYQ 295
Qy 310 --DISEQHISLDFGDPGRNHEMHCPRKHLPWPMTAITPSILVLVITFLVGYLYEAIN 367
Db 296 ECDTSLHESKLDGDPKPKHQMICRYHQKAPPSTALTATFAFFVIGLLVGYLYGAAT 355
Qy 368 RIATVEEDCQKRELKARAEADIAKSQFLATVSHIERTPMNGVLGMLMDTDLDAKQ 427
Db 356 HIVKVEDDFHEMQELKRAEAAADVAKSQFLATVSHIERTPMNGILGMLALLDTELSTQ 415
Qy 428 MDYATARGSGKDLTSLINEVLDOAKIESGRLEENVPDMRFILDNVSSLLSGKANBK 487
Db 416 RDYATQAIQKALIALINEVLDRAKIENGKLEETVPFDIRSILDDVLSFSESRRHG 475
Qy 488 TELAVYSSQVDDVVVGGPSRFRQIITNLVGNISIKFTQERGHIFISVHLADEVKEPLTI- 546
Db 476 TELAVFVADKPEIVMGDPGRFRQIITNLVGNISYKFT-EKGHIFVKVHLADQVKGATNAH 534
Qy 547 -----EDAVLKQRLALGCSSEGTVSQFPVAVNGSWKNFKTCYS-----586
Db 535 AKTCLNGRPERDILISDGSQ-----ETLSGCEVADERNSWDTFNLLVABDQFNSVDN 588
Qy 587 -TESQNSDOIKLVTYVDTGVGIPVDAQGRIFTFPMQADSTSRGTGGTGIGLSIKRLV 645
Db 589 MTSNEASENVVMVSVSDTGIGIPRAQDQRFVPMQADSTSRGTGGTGIGLSIKRLV 648
Qy 646 BLMQGEMGFVSEPGIGSTFSGTGVFGKAETNTSITKLERFDLAIQETGLRALVIDNRNI 705
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Db 649 ELMGCHINFI SRPQIGSTFTAVFGRCRLVFNVRKTFEDLPFGFKGLKAI VVDGKPV 708
QY 706 RAEVTRYELRLGISADIVSSLRMACTCCISKLENLA-----MILIDKXANNKEFSV 758
Db 709 RAAVTRYHLNRLGINVEVASSIN-AITATGKGKSLTAGYRHPDIILVEXDMW-----MSS 763
QY 759 LDEFT-----RSKVTRYRVPKIFLLATSLTERSEMKSTGLIDEVWIKPLRMSVLIC 812
Db 764 IDSWLSLTVDWKQGNLIQPKI-LLASKISASELEKAKASGADTVIMKPVASMLAA 822
QY 813 CLQETLVNGKR--QPNRQRN---LGHLEKQILVVDNLNRRVVAEGALKKYGAI 866
Db 823 CLQVLGIRGRKQLOKQDMNMGSSALRSLLYGKILVVDNKNRRVVAEGALKKFGANV 882
QY 867 TCVESGKAALAMKPPHNFDAFCFMDLQMPDMDGFEATRVRELEREINKKIASGEVSAEM 926
Db 883 ECASGKAALQLQPHDFDAFCFMDIOMPEMDGFEATRVRELEREINKKIASGEVSAEM 940
QY 927 FCKFSWHVPILAMTADVIQATHERCEMKGMDGYVSKPFEFEVLYTAVAREFF 978
Db 941 IVKGGEWHVPILAMTADVIQATHERCEMKGMDGYVSKPFEFEVLYTAVAREFF 992
RESULT 9
US-10-135-322-18
; Sequence 18, Application US/10135322
; Publication No. US20020173017A1
; GENERAL INFORMATION:
; APPLICANT: BENFEY, PN
; APPLICANT: HELARIUTTA, Y
; APPLICANT: MAHONEN, AP
; APPLICANT: BONKE, AMW
; APPLICANT: KAUPPINEN, L
; APPLICANT: RIIKONEN, M
; TITLE OF INVENTION: WOODEN LEG GENE, PROMOTER AND USES THEREOF
; FILE REFERENCE: 5914-086-999
; CURRENT APPLICATION NUMBER: US/10/135,322
; CURRENT FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: 60/253,739
; PRIOR FILING DATE: 2000-11-29
; NUMBER OF SEQ ID NOS: 43
; SOFTWARE: Patent in version 3.0
; SEQ ID NO 18
; TYPE: PRT
; ORGANISM: Arabidopsis thaliana
US-10-135-322-18
Query Match 51.7%; Score 2595.5; DB 14; Length 1092;
Best Local Similarity 55.0%; Pred. No. 2.6e-229;
Matches 538; Conservative 141; Mismatches 220; Indels 79; Gaps 14;
QY 35 WRKNLLILGILGVSFVSVMWVDWTEEMIKRRETLANMCDERARVLOQFNVSINHVA 94
Db 92 WRK-LVVVVVFWVLVSIWTFYFSQAMEKKEKELANMCDERARVLOQFNVSINHVA 150
QY 95 LSLVSTFHGKIPSAIDQRTFEYTERNFERTPLTSGVAYALKVPHSERKPEKHGWA 154
Db 151 MSILISTFHGKIPSAIDQRTFEYTERNFERTPLTSGVAYAMRVLHSEBEFERQGW 210
QY 155 IKKMETEDQTV--QDCVENFDPAIQDEYAPVIFAQTVSHIVSDMSGEEDRENIL 212
Db 211 IRKMYLEQNPHKDDYDLLEALPSPVQBEYAPVIFAQTVSHVSLDMSGEEDRENIL 270
QY 213 RARASGKGLVTPFKLLKSNHLGVLVLTFAVYDTSLPDATEQRVEATIGVLGASYDMP 272
Db 271 RARSSGKGLVTPFKLLKSNHLGVLVLTFAVYDTSLPDATEQRVEATIGVLGASYDMP 330
QY 273 LVEKLHLQASKQTIAVDYDTNTSGLIKMYGSGIGDISEOHISLDFGDPSPRNHEMH- 331
Db 331 LVENLLQLASKQTILVNVYDITNHSQPISMYGTNVSDGLERVSPLIFGDPRLKHEMRC 390

QY 332 -----CRFKHKLPIWTAITPISILVLTFTLVYGY 360
Db 391 RYLQLAHTVVCNFFLFARIQVLTFCCELLPLCRFPKPPWPLVSMVTSFGILVIALVAH 450
QY 361 ILYEAINRATVEEDCQKRELKABAEADIAKSQFLATVSHIETPNVGLKMLKMD 420
Db 451 ITHATVSRIRHVEEDCKMKQKKAEEADVAKSQFLATVSHIETPNVGLKMLKMD 510
QY 421 TOLDRAQMDYAOTAGSGKDLTSLNEVLDOAKIESGRLLELENVDFMRFLDNLVSSLLS 480
Db 511 TELDTVQDYVTAQASGKALVSLNEVLDOAKIESGRLLELENVDFMRFLDNLVSSLLS 570
QY 481 GKANEKIEBLAVYVSSQVDPVVDPSRFRQIITNLVGNISIKFTQERGHIFISVHLADEV 540
Db 571 SKSQKGVBLAVVSDRVPDMLIGDPRFRQIITNLVGNISIKFT-EGKHIFVTVHLVDEL 629
QY 541 KPLTITTEDAVLQRLALGSEGETVSGFPVAVNANGSMKNKFTCYSTESQNS-----DQI 595
Db 630 FSIDGETA-----SPSESTLSGLPVADRRORSWENFK-AFSSNGHRSFEPSPPDI 678
QY 596 KLLVTVVEDTGVGIPVDAQGRIFTFPMQADSSSTRYGTGTGIGLSISKRLVELMQGEMGFV 655
Db 679 NLIVSVEDTGVGIPVEAQSRIFTFPMQVGPSISRTHTGTTGIGLSISKRLVELMQGEMGFV 738
QY 656 SEPGIGSTFSTGVFG-----KAENTSTITKLERFDLAIQBFGLRALVIDNRNIRA 707
Db 739 STPKVGSTFTTAVFSGMGPAAERKNDNNQPI-----FSEFRGMKAVVVDHRPAPA 789
QY 708 EVTRYELRLGISADIVSSLRMACTCCISKLENLAMILIDKXANNKEFSVLDLFTSRK 767
Db 790 KVSWHYFQRLGIRVEVPRVEQALHYLKITVTVMILLIEQIWNREADDFIKKL---OK 846
QY 768 VTFTRYPKIFLLATSATLTERSEMKSTGLIDE--VVIKPLRMSVLICLQETLVNGKRQ 825
Db 847 DPLFLSPKILLANSVE-SSISEALCTG-IDPPIVIVKPLRASMLAATLQRLGIGIREP 904
QY 826 PRQ---RRNLGHLLREKQILVVDNLNRRVVAEGALKKYGAIIVCVESGKAALAMKPP 882
Db 905 PQHKGPALILRLNLLGRKILVVDNKNRRVVAEGALKKYGADVVCAESGKAIKSLKPP 964
QY 883 HNFDAFCFMDLQMPDMDGFEATRVRELEREINKKIASGEVSAEMFCKFSWHVPILAMTA 942
Db 965 HEEDACFMDIOMPEMDGFEATRVRELEREINKKIASGEVSAEMFCKFSWHVPILAMTA 1024
QY 943 DVIQATHECEMKGMDGY 960
Db 1025 DVIQATHECEMKGMDGY 1042
RESULT 10
US-09-918-508-6
; Sequence 6, Application US/09918508
; Patent No. US20020177162A1
; GENERAL INFORMATION:
; APPLICANT: KAKIMOTO, TATSUO
; APPLICANT: HIGUCHI, MASAYUKI
; APPLICANT: INOUE, TSUTOMU
; TITLE OF INVENTION: ANALYSIS OF AGONIST-ACTIVITY AND ANTAGONIST-ACTIVITY
; FILE REFERENCE: Q65478
; CURRENT APPLICATION NUMBER: US/09/918,508
; CURRENT FILING DATE: 2001-08-01
; PRIOR APPLICATION NUMBER: JP 2001-073812
; PRIOR FILING DATE: 2001-03-15
; NUMBER OF SEQ ID NOS: 22
; SOFTWARE: Patent in Ver. 2.1
; SEQ ID NO 6
; LENGTH: 1057
; TYPE: PRT
; ORGANISM: Arabidopsis thaliana
US-09-918-508-6
Query Match 50.7%; Score 2545.5; DB 10; Length 1057;

Best Local Similarity 53.3%; Pred. No. 9.9e-25;
Matches 538; Conservative 152; Mismatches 239; Indels 81; Gaps 17;

Qy	4	GERKEKHVLOE--ALAPKKQOORAQTSSRGAGRWKRKILLGLIGLIGVSFSYV-WFWDNE	60
Db	89	GNKKGSTFIOEHRALLPKAL-----ILWIIIVGFSSGIIQWDDANK	131
Qy	61	EIIWKRETLANMCDERARVLQDNVSLNHHVHLSILVSTFHGKIPSAIDQRTFEYIT	120
Db	132	---IRREBVLVSMCDQARMQLQDQFSVNVHVALAILVSTFHYHKNPASIDQETFAEYT	188
Qy	121	ERTNFERPLTSGVAYALKVPHSEBEKEKEHGWALKWETEDQTVQDCVPENFDPAIQ	180
Db	189	ARTAFERPLLSGVAYAEKVNFEREMFERQENWIKT-----DRGESPSPVR	235
Qy	181	DEYAPVIFAQTVSHIVSDMMGSEEDRENILRASGKGVLTSPFKLLKSNHLGVLT	240
Db	236	DEYAPVIFSQDSVSYLESLDMMGSEEDRENILRARETGKAVLTSPFRLLETHHLOVLT	295
Qy	241	AVYDTSLPDPATEQRVEATIGYLGASVDMPSLVEKLLHQLASKOTIAVDVYDTTNSGL	300
Db	296	PVYKSSLPENPTVBERIAATAGYLGGAQVDSLSVENILQLAGNQAIWVHVYDITNASDP	355
Qy	301	LKWYGS--EIGDISEQHISSIDFGDPSRNHEMHCFKHKLPIPWATATPSILVLVITFLV	358
Db	356	LVWYGNODEADRLSHESKLDGDPGRKKHKMICRYHQKAPIPLNVLTITVPLFAIGFLV	415
Qy	359	GYILYEAINRIATVEEDCQKRELKARAEAAIDAKSQFLATVSHERTPMGVLMGLKML	418
Db	416	GYILYGAAMIWKVEDDPHEMOELKVRAEADVAKSQFLATVSHERTPMNGILLOMLAML	475
Qy	419	MDTDLDAKMDYQATAHGSGKDLTSLINEVLDOAKIESGRLELBNVPFDMRFLDNYSSL	478
Db	476	LDTLSLSTORDYQATAQVCCKALITALINEVLDRAKIEBAGLELESVPFDIRSILDDVLSL	535
Qy	479	LSGKANEGHGLAVYVSSQVDPVVGDPSPRQIIITNLVGNISIKFTQERGHIFFISVHLAD	538
Db	536	FSESRNKGHGLAVFSDKVPFVIVKGSQGRQIIITNLVGNVSKFT-EKGGHIFVKVHLAE	594
Qy	539	EVK---EPL-TIEDAVLKQRLALGCSBSGETVSGFPVNAWGSKNFKTCVSTESQNSD-	593
Db	595	QSKDESEPKNALNGVSEEMIVVSKQSSYNTLSGYEADGRNSWDSEKHLVSEQSISEP	654
Qy	594	---QTKLLTVEDTGVGIPVDQAQRIPTFPQADSDSTSYTGGTGLSLSKRLVBLMQ	649
Db	655	DISNRLMWSIEDTGTGIPLVAGRVFMPFQADSDSTSYNGYGTGTGLSKCLVELMR	714
Qy	650	GEMGFVSEPGIGSTFPGVFGAETWTSITKLER--FDLAIQFTGLRALVITDNRIRA	707
Db	715	GQINFISRHIGSTFWFTAVLEKCDKCSAHHMKKNVNEHLPSTFGKMKAIIVDAKPVRA	774
Qy	708	EVTRYELRLRIGISADIVSSLRMACTCCISKLEN-----LAMILIDKAW-----NK	753
Db	775	AVTRYEMKRLGINVDVVVTSLKTAVAAAAAPERNGSPLPKTPQLDMLILVXDSMISTEDND	834
Qy	754	EEFSVLDELPTRSKVYFTRVPKIFLATSATLTERSEMKSTGLIDEVVIKPLMSVLICC	813
Db	835	SEIRLLNSR-TNGNV-HHKSPKIALFATNITNSEFDRAKSAGFADTVIMKPLRASMITGAC	892
Qy	814	LOETLVNGKKRQPNRORN--LGHILREKQIILVDDNLNRRVAREGALKKYGAIYTCVE	870
Db	893	LOQVLELRKTRQHPGSSSPATLKSLLTGKILVDDNI VNRVVAEGALKKFGAEVVCAE	952
Qy	871	SGKAAALAMLKPPHNFDACFMQLQMPEDMGFEATRRVRELEREINKKIASGEVSAEMPKF	930
Db	953	SGQVALGLLQIPHTFDACFMDIQMPQMDGFEATRQRMMEKAEKTN-----1000	
Qy	931	SSHWVPIIANTADYIOATHECKMCGMDGVVSPFBEVLVYTVARFPFEP	980
Db	1001	LEWHLPIIANTADYIHATYBECLKSGMDGVVSPFBEENLYKSVAKSFKP	1050

RESULT 11

Db 715 GQINFISPHIGSTFWTAFLVKCKDCSAINHMKPNVHLPSTFKGMKAIVVDAKPVRA 774
Qy 708 EVTRYELRLGISADIVSSLRMACTCCISKLEN-----LAMILIDKAW-----NK 753
Db 775 AVTRYHMKRLGINVDVTSKTAIVAAAFERNGSPFTKQDMLVLEKDSWISTEDND 834
Qy 754 EEFVSLDELFTRSKVTFTVRPKIFLIATSATITERSEMKSCTGLIDDEVVILKRLMSVLICC 813
Db 835 SEIRLLNSR-TNGNV-HHKSPKALFATNINSEFDRKASAGFADTVIMKPLRASMIGAC 892
Qy 814 LOETLVNGKQPNQRNRN---LGHLLREKQILVDDNLVNRVVAAGALKYKGAIVTCVE 870
Db 893 LOQVLELRKTRQOHPGEGSPATLKSLLTGKILVDDNLVNRVVAAGALKYKGAIVTCVE 952
Qy 871 SGKAALAMLKPPHNFDAFMDLQMPMDGFEATRRVRELEREINKKIASGVSABMFCKF 930
Db 953 SGQVALGLLQIPHTFDACFMDIOMPQMDGFEATRRVRELEREINKKIASGVSABMFCKF 1000
Qy 931 SSWHVPILAMTADVIQATHEECMKCMGMDGYVSKPFEELVYTAVARFPEP 980
Db 1001 LEWHLPIAMTADVIHATVECLKSGMDGYVSKPFEENLYKSAKSFKP 1050

RESULT 12

US-10-135-322-24
; Sequence 24, Application US/10135322
; Publication No. US20020173017A1
; GENERAL INFORMATION:
; APPLICANT: BENFEY, BN
; APPLICANT: HELARIUTTA, Y
; APPLICANT: MAHONEN, AP
; APPLICANT: BONKE, AMW
; APPLICANT: KAUPPINEN, L
; APPLICANT: RIIRONEN, M
; TITLE OF INVENTION: WOODEN LEG GENE, PROMOTER AND USES THEREOF
; FILE REFERENCE: 5914-086-999
; CURRENT APPLICATION NUMBER: US/10/135,322
; PRIOR FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: 60/253,739
; PRIOR FILING DATE: 2000-11-29
; NUMBER OF SEQ ID NOS: 43
; SOFTWARE: Patent in version 3.0
; SEQ ID NO 24
; LENGTH: 1057
; TYPE: PRT
; ORGANISM: Arabidopsis thaliana
US-10-135-322-24

Query Match 50.6%; Score 2539.5; DB 14; Length 1057;
Best Local Similarity 53.2%; Pred. No. 3.5e-224;
Matches 537; Conservative 152; Mismatches 240; Indels 81; Gaps 17;
Qy 4 GERKEKVLQGE--ALAPKQOQQAQTSRRGAGRWKRNILLGLGVSFSVW-FWWDNNE 60
Db 89 GNKKGTFQERHALIPKAL-----LWIIIVGFISSGIYQWDDANK 131
Qy 61 EITMKRETLANCDEARVLOQFNVSNLHVLSILVSTPHHGKIPSAIDQRTFEYT 120
Db 132 ---IRREEVLVSCDQARMQDOFVSQVSNVHVALAILVSTPHYHKNPSAIDQRTFEYT 188
Qy 121 ERNFRPLTSGYAYALKVPHSREKFEKHEGWAIKKMETEDQTVVQDCVPENFQAPIQ 180
Db 189 ARTAFERPLLSGAYAKVKNVFNFERFQHNVIKTM-----DRGEFSPVR 235
Qy 181 DEYAPVIFAQETVSHVSVDMMSGEEDRENILRARASGKVLTPPKLKSNNHGLVLTFF 240
Db 236 DEYAPVIFSQDSVSYLSLDMMSGEEDRENILRETRGKAVLTSPRLLETHLGLVLTFF 295
Qy 241 AVYDTSLPDPATBEORVEATIGYLGASVDMPSLVKLLHQLASKQTIADVVDYDTNTSGL 300
Db 296 FVYKSSILPENPTVEERIAATAGYLGAFDVSILVNLGLAGNQAIVVHVVDITNASDP 355

Qy 301 IKMNGS--BIGDISEOHISLSDPGSPRNHMEHCRFKHKLPIPTAITPSILVLVITVELV 358
Db 356 LVMYGNQDEADRSLSHESKLDGDFPRKHKMICRYHQKAPIPNLVLTPTVPLFFAIGELV 415
Qy 359 GYLYEAINRIATVEEDCOKMELKARABAAADIAKSOFLATVSHETRTMNGVILGMLKWL 418
Db 416 GYLYGAAMHI VKVEDDFHEMQELKVRABAAADVAKSOFLATVSHETRTMNGVILGMLKWL 475
Qy 419 MDTDLDAKQMDYAQTAGHSGKDLTSLINEVLVDAQIESGRLEENVPFDMREILDNVSSL 478
Db 476 LDTLELSSITQDQYATQAVCGKALIALINEVLVDRAKIEAGKLELESVPPDIRSILDVLSL 535
Qy 479 LSKANEKEGIELAVYSSQVDPVVVGDPSRFQIITNLVGNISIKTQERCHTIFISVHLAD 538
Db 536 FSESENKSIELAVFVSDKVPFVIRVGRFQIITNLVGNISIKTQERCHTIFISVHLAD 594
Qy 539 EVK---EPL-TTIEDAVLKORLALGCSGETVSGFPAVNAWGNKFNKTCYTESQNSD- 593
Db 595 QSKDESEPKNALGVSEEMIVVSKOSSYNTLSGYEADGRNSWDSFKHLVSEEQSLSEF 654
Qy 594 ----QIKLLVTVEDTGVGIPVDAQGRIFTPFMOADSSTRTYGGTGIGLSISKRLVELMQ 649
Db 655 DISSNVLVMSIEDTGIGIPVDAQGRVFPFMOADSSTRTYGGTGIGLSISKRLVELMR 714
Qy 650 GENGVSSEPGIGSTFSTFTGVFGKAEINTSITKLER--FDLAIQEFITGLBALVIDNPNRA 707
Db 715 GQINFISPHIGSTFWTAFLVKCKDCSAINHMKPNVHLPSTFKGMKAIVVDAKPVRA 774
Qy 708 EVTRYELRLGISADIVSSLRMACTCCISKLEN-----LAMILIDKAW-----NK 753
Db 775 AVTRYHMKRLGINVDVTSKTAIVAAAFERNGSPFTKQDMLVLEKDSWISTEDND 834
Qy 754 EEFVSLDELFTRSKVTFTVRPKIFLIATSATITERSEMKSCTGLIDDEVVILKRLMSVLICC 813
Db 835 SEIRLLNSR-TNGNV-HHKSPKALFATNINSEFDRKASAGFADTVIMKPLRASMIGAC 892
Qy 814 LOETLVNGKQPNQRNRN---LGHLLREKQILVDDNLVNRVVAAGALKYKGAIVTCVE 870
Db 893 LOQVLELRKTRQOHPGEGSPATLKSLLTGKILVDDNLVNRVVAAGALKYKGAIVTCVE 952
Qy 871 SGKAALAMLKPPHNFDAFMDLQMPMDGFEATRRVRELEREINKKIASGVSABMFCKF 930
Db 953 SGQVALGLLQIPHTFDACFMDIOMPQMDGFEATRRVRELEREINKKIASGVSABMFCKF 1000
Qy 931 SSWHVPILAMTADVIQATHEECMKCMGMDGYVSKPFEELVYTAVARFPEP 980
Db 1001 LEWHLPIAMTADVIHATVECLKSGMDGYVSKPFEENLYKSAKSFKP 1050

RESULT 13

US-10-126-120-2
; Sequence 2, Application US/10126120
; Publication No. US20030108526A1
; GENERAL INFORMATION:
; APPLICANT: Sakakibara, Hitoshi
; APPLICANT: Takei, Kentaro
; TITLE OF INVENTION: MICROORGANISMS FOR USE IN THE MEASUREMENT OF ENVIRONMENTAL FACTO
; FILE REFERENCE: 11127-004001
; CURRENT APPLICATION NUMBER: US/10/126,120
; PRIOR FILING DATE: 2002-04-19
; PRIOR APPLICATION NUMBER: JP 2001-291059
; PRIOR FILING DATE: 2001-09-25
; NUMBER OF SEQ ID NOS: 50
; SOFTWARE: Patent in ver. 2.1
; SEQ ID NO 2
; LENGTH: 974
; TYPE: PRT
; ORGANISM: Zea mays
US-10-126-120-2

Query Match 47.1%; Score 2363; DB 15; Length 974;
Best Local Similarity 50.8%; Pred. No. 5.6e-208;
Matches 503; Conservative 152; Mismatches 251; Indels 84; Gaps 18;

QY	34	RWRKNILLIG-ILGGVSPSVMMFWMDTNEEIIIMKRETLAMCDEARVLQDOFNYSLNHV	92
Db	:	: :	:
Db	12	RWNRGLAAAGWVLTAVWCASVMHMTLRDRSDMRAERLVSMCBERRMLQEFGVTNVHV	71
QY	93	HALSILVSTPHHGKIPSAIDORTPEETERNRPERLITSGVAYALKVPHSEREKTEKHG	152
Db	72	HAIALIISTFNFKEKPPAIDOOTFAKYTARTSFERPPLNGVAFAQRVFHHEREMFSQG	131
QY	153	WAIKOMETDQTVDQCPENFPDPAPIODEYAPVIFAQETVSHIVSVMMSGEEDRENIL	212
Db	132	VWNWTMORE-----PAPPQVEYAPVIFSQDTVSYLARDMMSSGEEDRENIF	177
QY	213	BARASKGVLTSPFFKLKSNHLGVLTFAVYDTSLPDATABORVEATTGYLGASVDMPS	272
Db	178	RARTTGKALTNPFRLLGNHLGVVLTFAVVRPDLPADASVEQRVEATIGYLGAFDVBS	237
QY	273	LVEKLHLQLASQTTIAVDYDITNTSGLIKWGSEIGDISEQ----HISSLDFGDP SRNH	328
Db	238	LVENLLSKLAGNQDIVNNVYDVYNASDAWLYGP--SSLDEQPFFLHVMSLMDFGDPRKH	295
QY	329	EMHCRRPKHLPWPWTAITPSLIVLVIPTFLVGYILIYEAINRIATVEBDCQORRLKARAB	388
Db	296	EMCRRYRQLKPWFSAITNPLGTFIWMLLGYSAAAYSRYDKVTEDCKMEELKTQABA	355
QY	389	ADIAKSOFLATVSHERTPMNGVIGMLKOLAMDOLDAKOMDYAQTAGSGKOLTSLINEV	448
Db	356	ADVAKSOFLATASHERTPMNGVIGMLDMLLGTDLTMTQDXACTACMQCGRALLITLINDV	415
QY	449	LDQAKTESGRLEHENVPFMRFILDNVASLISGKANEGKIELAVYVSSQVDDVVGDPRS	508
Db	416	LDRAKTEAGKLEAVEPFDRLSDMDVNSLFSKSRKENCIEIAVFCDNVPKVVI G D P W R	475
QY	509	FROIITNLVGNSTKFTOERGHFIISVHLADEVKPLETTIDAVALKORLALCSBSGS---	564
Db	476	FROIITNLVGNAVKT-EGHFVFAVCIA-----ENSMEANQVTLHGANGKGGRV	525
QY	565	-----TVSGFPVANAWGSKNFKTCYS-----TESQN-----SDQIKLLVTVE	602
Db	526	ESTANGAFNTLSGFEAADRNRNSQVFKLLSDSKESLDDLDESNSQSDSDRVTLAISIE	585
QY	603	DTGVGTPVDAQRI FTPEMOADSSTRYTGGTIGLSTISKRLVELMOGEMGFVSEPIGS	662
Db	586	DTGVGTPLOQDRVTFPFMAOSDSTRYGGTIGLSTISKCLAEIMGGOJSTFTHSPVSGS	645
QY	663	TFSFTGVPGKAENTSI TKLERFDLAI-QEFTGLRALVIDNRINRAETRYELLERLGISA	721
Db	646	TFTFSATLKSHKDISGDSRSRLTEALPTAFKMGKAILVDGRPVRSATVRYHLKRLGILL	705
QY	722	DIYSSLRMACTC-----CISKLENIAMLLDKDANKKE-EFVSDELFLTFSKVTTRVP	774
Db	706	QVNMMNAVVKAPFGONGAAGSREKASILFTESDPWRPETDVDQLNLHRSKQNGQUSDGH	765
QY	775	KIFLLATSATLTERSEMKGTLIDEVTKPLRMSVLIICLOETL-VNGKRQPNRQRN-	832
Db	766	KVVLVTS---EADKDKYGSIFDIVMCKPIRASTIASIQQLLKVEIERKDQNRPSF	821
QY	833	LGHLLREKQILVDDNLNRRVARBGALKYGIATVTCVESGXAALAMLKPHNFEDACFMDL	892
Db	822	LRSLLVGKNTILVDDNKVLRVAAAALKKYGANSCVSGDKDAISLIQQPHRFDACFMDV	881
QY	893	QMPMDGFEATRVRRELERINK---KIAS--GVVSABMFCKFSWHVPILTAMTADVIQ	946
Db	882	QMPMDGFEATGQIRQMELKANEERNKULASTEGSTTAE-----YHLPVLTAMTADVIQ	934
QY	947	ATHEECMKGMGCVGVSKEPBEENVLYTAVAR	976
Db	935	ATYBECTKSGMDGVGVSKEPDEEQLYQAVSR	964

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; Publication NO. US20030046728A1
;
; GENERAL INFORMATION:
; APPLICANT: Strabala, Timothy
; APPLICANT: Nieuwenhuizen, Nicolaas
; APPLICANT: Higgins, Colleen M.
; TITLE OF INVENTION: Compositions Isolated from Plant Cells
; TITLE OF INVENTION: and Their Use in the Modification of Plant Cell Signaling
; FILE REFERENCE: 11000.1020c2
; CURRENT APPLICATION NUMBER: US/10/101,464A
; CURRENT FILING DATE: 2002-03-18
; PRIOR APPLICATION NUMBER: 09/704,302
; PRIOR FILING DATE: 2000-11-01
; PRIOR APPLICATION NUMBER: 09/228,986
; PRIOR FILING DATE: 1999-01-12
; PRIOR APPLICATION NUMBER: 60/162,866
; PRIOR FILING DATE: 1999-11-01
; PRIOR APPLICATION NUMBER: PCT/US00/00724
; PRIOR FILING DATE: 2000-01-11
; NUMBER OF SEQ ID NOS: 989
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 978
; LENGTH: 480
; TYPE: PRT
; ORGANISM: Eucalyptus grandis
; US-10-101-464A-978

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Query Match 27.5%; Score 1378; DB 15; Length 480;
Best Local Similarity 58.9%; Pred. No. 9.3e-118;
Matches 282; Conservative 67; Mismatches 110; Indels 20; Gaps 3;

Qy	10	VHLQBALAPKXQOQRAQTSSRGAGRMKNTILLGILGVSVFVWVFWDTNBEIIMKRRET	69
Db	14	VKLNBEQVGTK---RGVTFIQSNRAWTPKILVLISVVGVMAFLSMSYRKMDADIKVRRKEV	69
Qy	70	LANNMDEARVLQDQFNYSLNHVALSILVSTPHGKI PSAIDORTFEERTTFRPL	129
Db	70	LYSVMCQQRARMLKQFVSVMNHVALAILVSTHYKNPSAIDQETFBYRTARTAFRPL	129
Qy	130	TSGVAYALKVPHSREKFEKEHGWAIKMBETEDQTVVQCPVENFDPAPIDQEYAPVIPA	189
Db	130	LSGVAVAEVRTNSREKFEQHGWTIKMEKQ-----PSPVRDEYAPVIFS	175
Qy	190	QETVSHIVSDMMSGEEDRENILPARASGKVLTSPFKLLKNHGLVLTFRAYDTSIPP	249
Db	176	QETVSYSIELDMMSGEEDRENILARATGKAVITSPFRLLGSHLGVLTFFVYKSKLPP	235
Qy	250	DATEORVEATIGYLGASYDMPSLVEKLLHQLASKOTIAVDVYDNTTSGLLIKMYGSEIG	309
Db	236	NPTVBERIEATVYLGAGFVSESVLENLLQDQCNQAILVWYDVYDINSSEPLMYGHQVQ	295
Qy	310	--DISEQHISLDFDQPSRNEHMCRPKHKLPIPTWATIPSLIVLVTITFLGVYIYBAIN	367
Db	296	ECDTSLHSEKSLDFDQPPFRKHQMTCRYHQKAPPSWTALTAPFPVFIGLVGLYIILYGAAT	355
Qy	368	RIATVEEDCQKRELKARAEAAIDAKSOFLATYSHEIRTPMNGVLQMLKMLMDTOLDRAQ	427
Db	356	HIVKVEDDPHEQELKVRAEAAADWAKQFLATYSHEIRTPMNGILQMLALLDTELSTQ	415
Qy	428	MDYACPTAGSGKDLTSLINEVLQAKIESCRLELENVFFDMRPILDNVSLLSGKANEX	486
Db	416	RDYACPTACGKAILALINEVLDRAKTEAGKILETVPFDIRSLIDVLSTLSESRHK	474

RESULT 15

```

RESUME 15
US-101-464A-124
; Sequence 124, Application US/10101464A
; Publication No. US20030046728A1
; GENERAL INFORMATION:
; APPLICANT: Strabala, Timothy
; APPLICANT: Nieuwenhuizen, Nicolaas
; APPLICANT: Higgins, Colleen M.
; TITLE OF INVENTION: Compositions Isol
; TITLE OF INVENTION: and Their Use in

```


GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: November 28, 2003, 13:58:54 ; Search time 32.8827 Seconds
(without alignments)
7698.569 Million cell updates/sec

Title: US-09-918-508-2_COPY_196_1176

Perfect score: 5019

Sequence: 1 KARGERKEVHLQALAPKK.....SKPFEELVYTAARFFEPFC 981

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 830525 seqs, 258052604 residues

Total number of hits satisfying chosen parameters: 830525

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

SPTREMBL 23:*

- 1: sp_archaea:*
- 2: sp_bacteria:*
- 3: sp_fungi:*
- 4: sp_human:*
- 5: sp_invertebrate:*
- 6: sp_mammal:*
- 7: sp_mhc:*
- 8: sp_organelle:*
- 9: sp_phase:*
- 10: sp_plant:*
- 11: sp_rodent:*
- 12: sp_virus:*
- 13: sp_vertebrate:*
- 14: sp_unclassified:*
- 15: sp_rvirus:*
- 16: sp_bacteriap:*
- 17: sp_archaeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	5019	100.0	1176	10 Q9C5U2	Q9C5U2 arabidopsis
2	4991.5	99.5	1173	10 Q9FKH3	Q9FKH3 arabidopsis
3	3316	66.1	652	10 Q8GUG0	Q8GUG0 arabidopsis
4	3297.5	65.7	1041	10 Q8L8I6	Q8L8I6 catharanthus
5	2685.5	51.7	1036	10 Q9C5U1	Q9C5U1 arabidopsis
6	2595.5	51.5	1092	10 Q9FPK3	Q9FPK3 arabidopsis
7	2575	51.3	1023	10 Q8RYG4	Q8RYG4 oryza sativ
8	2545.5	50.7	1057	10 Q9C5T8	Q9C5T8 arabidopsis
9	2545.5	50.7	1080	10 Q9C5T8	Q9C5T8 arabidopsis
10	2539.5	50.6	1057	10 Q9S1T0	Q9S1T0 arabidopsis
11	2539.5	50.6	1080	10 Q9C5U0	Q9C5U0 arabidopsis
12	2520	50.2	925	10 Q8S6P5	Q8S6P5 oryza sativ
13	2363	47.1	974	10 Q9FY7	Q9FY7 zea mays (m
14	1125	22.4	627	10 Q9AUQ0	Q9AUQ0 oryza sativ
15	791	15.8	1765	16 Q8E1I0	Q8E1I0 shewanella
16	786.5	15.7	1417	16 Q9HWR8	Q9HWR8 pseudomonas

17	784	15.6	1268	2	Q8KQV0	Q8KQV0 vibrio chol
18	782	15.6	2062	5	Q95PH6	Q95PH6 dictyosteli
19	778.5	15.5	1261	16	P73266	P73266 synchocyst
20	776	15.5	1331	16	Q9KSB0	Q9KSB0 vibrio chol
21	775	15.4	1320	16	Q8D5E0	Q8D5E0 vibrio chol
22	765	15.2	1353	16	Q8DJB3	Q8DJB3 synchococc
23	761	15.2	1299	16	Q8YUQ6	Q8YUQ6 anabaena sp
24	760	15.1	1364	16	Q8P883	Q8P883 xanthomonas
25	759.5	15.1	1364	16	Q8P883	Q8P883 xanthomonas
26	758	15.1	1550	16	Q8YUQ8	Q8YUQ8 anabaena sp
27	756.5	15.1	1072	16	Q8D7S2	Q8D7S2 vibrio vuln
28	753.5	15.0	1462	16	P73035	P73035 synchocyst
29	751	15.0	928	16	Q8DC68	Q8DC68 vibrio vuln
30	743.5	14.8	1817	16	Q8YU51	Q8YU51 anabaena sp
31	740.5	14.8	1188	16	Q8EJ91	Q8EJ91 shewanella
32	739	14.7	1000	17	Q8TPA1	Q8TPA1 methanosaar
33	731.5	14.6	1298	3	Q01318	Q01318 neurospora
34	731	14.6	1307	3	Q9C1U1	Q9C1U1 magnaporthe
35	725.5	14.5	786	16	Q98FG5	Q98FG5 rhizobium 1
36	725.5	14.5	1035	16	Q8DKI3	Q8DKI3 synchococc
37	725	14.4	1243	16	Q8UC26	Q8UC26 agrobacteri
38	723.5	14.4	1315	3	Q8X215	Q8X215 botrytis ci
39	723.5	14.4	1315	3	Q8X1E7	Q8X1E7 botrytis ci
40	721.5	14.4	801	3	Q9UUN8	Q9UUN8 nectria hae
41	721.5	14.4	919	16	Q9HYE4	Q9HYE4 pseudomonas
42	721	14.4	1283	3	Q94094	Q94094 nectria hae
43	720.5	14.4	1298	3	Q01309	Q01309 neurospora
44	717	14.3	935	16	Q8F370	Q8F370 leptospira
45	715	14.2	925	16	Q31138	Q31138 pseudomonas

ALIGNMENTS

RESULT 1

Q9C5U2 ID Q9C5U2 PRELIMINARY; PRT; 1176 AA.

AC Q9C5U2; 01-JUN-2001 (TREMELrel. 17, Created)

DT 01-JUN-2001 (TREMELrel. 17, Last sequence update)

DT 01-MAR-2003 (TREMELrel. 23, Last annotation update)

DE Histidine kinase.

GN AHK2.

OS Arabidopsis thaliana (Mouse-ear cress).

OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;

OC eurosids II; Brassicales; Brassicaceae; Arabidopsi.

OX NCBI_TaxID=3702;

RN [1]

RP SEQUENCE FROM N.A.

RX MEDLINE=21154803; PubMed=11230578;

RA Asguchi C., Koizumi H., Suzuki T., Mizuno T.;

RT "Novel family of sensor histidine kinase genes in Arabidopsis

RL Plant Cell Physiol. 42:231-235(2001).

DR ENBL; AB046869; BAB40774.1; -

DR HSSP; P06143; 1AB6.

DR InterPro; IPR003594; ATPbind_ATPase.

DR InterPro; IPR006189; CHASE.

DR InterPro; IPR003661; His_kin.

DR InterPro; IPR005467; His_kinase.

DR InterPro; IPR001789; Response_reg.

DR Pfam; PF03924; CHASE; 1.

DR Pfam; PF02518; HATPase_c; 1.

DR Pfam; PF00512; HiskA; 1.

DR Pfam; PF00072; response_reg; 1.

DR ProDom; PD000039; Response_reg; 1.

DR SMART; SM00387; HATPase_c; 1.

DR SMART; SM00368; HiskA; 1.

DR SMART; SM00448; REC; 1.

DR PROSITE; PS50839; CHASE; 1.

DR PROSITE; PS50109; HIS_KIN; 1.

DR PROSITE; PS50110; RESPONSE_REGULATORY; 1.

KW Kinase; Phosphorylation; Sensory transduction.
SQ SEQUENCE 1176 AA; 131859 MW; AC0019CC612361BC CRC64;

Query Match 100.0%; Score 5019; DB 10; Length 1176;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 981; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KARGERKEKVLQALAPKQKQQAQTSRRGAGRWKRNILLGLGVSFVWFWDTNE 60
DB 196 KARGERKEKVLQALAPKQKQQAQTSRRGAGRWKRNILLGLGVSFVWFWDTNE 255
QY 61 EIMKRETLANMCDERARVLQDFNVSLNHVHLSILVSTFHHGKIPSAIDQRTFEYT 120
DB 256 EIMKRETLANMCDERARVLQDFNVSLNHVHLSILVSTFHHGKIPSAIDQRTFEYT 315
QY 121 ERTNFERPLTSGVAYALKVPHSEREKPEKHGWAIKKMETEDQTVVQDCVPEPDFPAPIQ 180
DB 316 ERTNFERPLTSGVAYALKVPHSEREKPEKHGWAIKKMETEDQTVVQDCVPEPDFPAPIQ 375
QY 181 DEYAPVIFAQETVSHIYVSDVMMSGEEDRENILRARASGKGLVTSPPFKLLKSNHLGVLTTF 240
DB 376 DEYAPVIFAQETVSHIYVSDVMMSGEEDRENILRARASGKGLVTSPPFKLLKSNHLGVLTTF 435
QY 241 AVYDTSPPDATERQORVEATIGYLGSYDMPSLVEKLLHQLASKQTTAVDVYDTTNTSGL 300
DB 436 AVYDTSPPDATERQORVEATIGYLGSYDMPSLVEKLLHQLASKQTTAVDVYDTTNTSGL 495
QY 301 IKMYGSEIGDISEQHISLSDGDSRNHEMCRFKHLPIPWTAITPSILVLVITFLVGY 360
DB 496 IKMYGSEIGDISEQHISLSDGDSRNHEMCRFKHLPIPWTAITPSILVLVITFLVGY 555
QY 361 ILYEAINRIATVEEDCQKRELKARAAADIAKQFLATVSHIERTPMNGVLGMLKMLMD 420
DB 556 ILYEAINRIATVEEDCQKRELKARAAADIAKQFLATVSHIERTPMNGVLGMLKMLMD 615
QY 421 TDLDAKQMDYAQTAHSGSKOLTSLINEVLDQAKIESGRLELENVPPDMRFTLDNVSSLLS 480
DB 616 TDLDAKQMDYAQTAHSGSKOLTSLINEVLDQAKIESGRLELENVPPDMRFTLDNVSSLLS 675
QY 481 GKANEKGIELAVYSSQVDPVVVGDPSRFRQIITNLVGNSTKFTQERGHIFISVHLADEV 540
DB 676 GKANEKGIELAVYSSQVDPVVVGDPSRFRQIITNLVGNSTKFTQERGHIFISVHLADEV 735
QY 541 KEPLTIEDAVLKQRLALGCSSEGETVSGFPVAVNAGSWKNFKTCYSTESQNSDQIKLVT 600
DB 736 KEPLTIEDAVLKQRLALGCSSEGETVSGFPVAVNAGSWKNFKTCYSTESQNSDQIKLVT 795
QY 601 VEDTGVGIPVDAQGRIFTFFPMQADSSTRTYGGTGIGLSISKRLVELMQGEMGFVSEPGI 660
DB 796 VEDTGVGIPVDAQGRIFTFFPMQADSSTRTYGGTGIGLSISKRLVELMQGEMGFVSEPGI 855
QY 661 GSTSFCTGFGKAEINTSITKLERFDLAIQFTGLRALVINDNRNIRAEVTRYELRLGLIS 720
DB 856 GSTSFCTGFGKAEINTSITKLERFDLAIQFTGLRALVINDNRNIRAEVTRYELRLGLIS 915
QY 721 ADVSSLSRMACTCCISKLENLAMILIDKAWNKEEFSVLDELFTRSKVTFTVRPKIFLLA 780
DB 916 ADVSSLSRMACTCCISKLENLAMILIDKAWNKEEFSVLDELFTRSKVTFTVRPKIFLLA 975
QY 781 TSATLTERSEMKSTGLIDDEVVIKPLRMSVLICCLQETLVNGKKQPNQRNHLGLLREK 840
DB 976 TSATLTERSEMKSTGLIDDEVVIKPLRMSVLICCLQETLVNGKKQPNQRNHLGLLREK 1035
QY 841 QILVVDNINVRVAEGALKKYGAIVTCVESGKAALAMLKPPHNFDACFMDLQMPMDGF 900
DB 1036 QILVVDNINVRVAEGALKKYGAIVTCVESGKAALAMLKPPHNFDACFMDLQMPMDGF 1095
QY 901 EATRVRELEREINKKIASGEVSAEMFCKFSSWHVPILAMTADVILQATHEECMKCGMDGY 960
DB 1096 EATRVRELEREINKKIASGEVSAEMFCKFSSWHVPILAMTADVILQATHEECMKCGMDGY 1155
QY 961 VSKPFEFEEVLYTAVARFPFPC 981
|||||

DB 1156 VSKPFEFEEVLYTAVARFPFPC 1176

RESULT 2
QYFKH3 PRELIMINARY; PRT; 1173 AA.

AC Q9FKH3
DT 01-MAR-2001 (TEMBLrel. 16, Created)
DT 01-MAR-2001 (TEMBLrel. 16, Last sequence update)
DT 01-MAR-2003 (TEMBLrel. 23, Last annotation update)
DE Histidine kinase-like protein.
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eurosid II; Brassicales; Brassicaceae; Arabidopsis.
OX NCBI_TaxID=3702;
[1]
RP SEQUENCE FROM N.A.
RC STRAIN=Columbia;
RX MEDLINE=98344145; PubMed=9679202;
RA Kaneko T., Kotani H., Nakamura Y., Sato S., Asamizu E., Miyajima N.,
Tabata S.
RT "Structural analysis of Arabidopsis thaliana chromosome 5. V. Sequence
features of the regions of 1,381,565 bp covered by twenty one
physically assigned P1 and PAC clones."
RL DNA Res. 5:131-145 (1998).
DR EMBL; AB011485; BAB09274.1; -.
DR HSSP; P06143; IAB6.
DR InterPro; IPR003594; ATPbind ATPase.
DR InterPro; IPR004358; Bact_sens_dr_C.
DR InterPro; IPR006189; CHASE.
DR InterPro; IPR003661; His_kinA.
DR InterPro; IPR005467; His_kinase.
DR InterPro; IPR001789; Response_reg.
DR Pfam; PF02518; HATPase_c; 1.
DR Pfam; PF00512; HiskA; 1.
DR Pfam; PF00072; response_reg; 1.
DR PRINTS; PR00344; BCTRLSENSOR.
DR ProDom; PD000039; Response_reg; 1.
DR SMART; SM00387; HATPase_c; 1.
DR SMART; SM00388; HiskA; 1.
DR SMART; SM00448; REC; 1.
DR PROSITE; PS00839; CHASE; 1.
DR PROSITE; PS0109; HIS_KIN; 1.
DR PROSITE; PS0110; RESPONSE_REGULATORY; 1.
KW Kinase; Phosphorylation; Sensory transduction.
SQ SEQUENCE 1173 AA; 131483 MW; 5FC6BAF0848PD1B2 CRC64;

Query Match 99.5%; Score 4991.5; DB 10; Length 1173;
Best Local Similarity 99.7%; Pred. No. 0;
Matches 978; Conservative 0; Mismatches 0; Indels 3; Gaps 1;

QY 1 KARGERKEKVLQALAPKQKQQAQTSRRGAGRWKRNILLGLGVSFVWFWDTNE 60
DB 196 KARGERKEKVLQALAPKQKQQAQTSRRGAGRWKRNILLGLGVSFVWFWDTNE 255
QY 61 EIMKRETLANMCDERARVLQDFNVSLNHVHLSILVSTFHHGKIPSAIDQRTFEYT 120
DB 256 EIMKRETLANMCDERARVLQDFNVSLNHVHLSILVSTFHHGKIPSAIDQRTFEYT 315
QY 121 ERTNFERPLTSGVAYALKVPHSEREKPEKHGWAIKKMETEDQTVVQDCVPEPDFPAPIQ 180
DB 316 ERTNFERPLTSGVAYALKVPHSEREKPEKHGWAIKKMETEDQTVVQDCVPEPDFPAPIQ 375
QY 181 DEYAPVIFAQETVSHIYVSDVMMSGEEDRENILRARASGKGLVTSPPFKLLKSNHLGVLTTF 240
DB 376 DEYAPVIFAQETVSHIYVSDVMMSGEEDRENILRARASGKGLVTSPPFKLLKSNHLGVLTTF 435
QY 241 AVYDTSPPDATERQORVEATIGYLGSYDMPSLVEKLLHQLASKQTTAVDVYDTTNTSGL 300
DB 436 AVYDTSPPDATERQORVEATIGYLGSYDMPSLVEKLLHQLASKQTTAVDVYDTTNTSGL 495

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QY 301 IKMYGSEIGDIHQHISLDFDGPDSRNHEHCHCFKHKLPIPWTAITPSSILVLVITFLVGY 360
DB 496 IKMYGSEIGDIHQHISLDFDGPDSRNHEHCHCFKHKLPIPWTAITPSSILVLVITFLVGY 555
QY 361 ILYEALNRIATVEEDCQKRELKARAEADIAKSQFLATVSHIEIRTPMNGVLGMLKMLMD 420
DB 556 ILYEALNRIATVEEDCQKRELKARAEADIAKSQFLATVSHIEIRTPMNGVLGMLKMLMD 615
QY 421 TDLDAKOMDYAQAHAHSGKDLTSLINEVLDQAKIESGRLELENVPPDMRFILDNVSSLS 480
DB 616 TDLDAKOMDYAQAHAHSGKDLTSLINEVLDQAKIESGRLELENVPPDMRFILDNVSSLS 675
QY 481 GRANEKIELAVVSVQPDVVGDPDSRRPQIITNLVGNISIKFTQERGHIFISVHLADEV 540
DB 676 GRANEKIELAVVSVQPDVVGDPDSRRPQIITNLVGNISIKFTQERGHIFISVHLADEV 732
QY 541 KEPLTTIEDAVLKORLALGSESEGETVSGPPAVNANGSWKNFKTCYTESQNSDOIKLVT 600
DB 733 KEPLTTIEDAVLKORLALGSESEGETVSGPPAVNANGSWKNFKTCYTESQNSDOIKLVT 792
QY 601 VEDTGVGIPVDAQGRIFTFPMQADSSTRTYGTGIGLSISKRLVELMQEMGFVSEPGI 660
DB 793 VEDTGVGIPVDAQGRIFTFPMQADSSTRTYGTGIGLSISKRLVELMQEMGFVSEPGI 852
QY 661 GSTFSFTGVPGKAEATNTSITKLERFDLAIQEFTGLRALVIDNRIAEVTRVRLRLGIS 720
DB 853 GSTFSFTGVPGKAEATNTSITKLERFDLAIQEFTGLRALVIDNRIAEVTRVRLRLGIS 912
QY 721 ADIVSSLRMACTCCISKLENLAMILIDKAWNKEEFSVLDLFTRSKVTFTRPVKIFLLA 780
DB 913 ADIVSSLRMACTCCISKLENLAMILIDKAWNKEEFSVLDLFTRSKVTFTRPVKIFLLA 972
QY 781 TSATLTERSEMSKSTGLIDEVVIKPLRMSVLICCLQETLVNGKKRQPNRQRLNHLRLREK 840
DB 973 TSATLTERSEMSKSTGLIDEVVIKPLRMSVLICCLQETLVNGKKRQPNRQRLNHLRLREK 1032
QY 841 QILVNDNLNRRVAEGALKKYGAIVTCVESGKAALAMKPPNFACFMDLQMPMDGF 900
DB 1033 QILVNDNLNRRVAEGALKKYGAIVTCVESGKAALAMKPPNFACFMDLQMPMDGF 1092
QY 901 EATRRVRELEREINKKIASGEVSAEMFCFSSWHVPILAMTADVIQATHECMKCGMDGY 960
DB 1093 EATRRVRELEREINKKIASGEVSAEMFCFSSWHVPILAMTADVIQATHECMKCGMDGY 1152
QY 961 VSKPFEEVLYTAVARFFEP 981
DB 1153 VSKPFEEVLYTAVARFFEP 1173

RESULT 3
Q8GUGO
ID Q8GUGO PRELIMINARY; PRT; 652 AA.
AC Q8GUGO;
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Histidine kinase-like protein.
GN AT5G35750.
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eurosids II; Brassicales; Brassicaceae; Arabidopsids.
OX NCBI_TaxID=3702;
RN [1]
RP SEQUENCE FROM N.A.
RA Southwick A., Nguyen M., Tripp M., Palm C.J., Jones T., Wu T.,
RA Carninci P., Hayashi K., Cheuk R., Chan M.M., Chang C.H., Dale J.M.,
RA Deng J.M., Hayashizaki Y., Hsuan V.W., Lee J.M., Ishida J., Kamiya A.,
RA Kawai J., Kim C.J., Narusaka M., Onodera C.S., Quach H.I., Sakurai T.,
RA Satou M., Seki M., Shinn P., Tang C.C., Toroumi M., Wong C., Wu H.C.,
RA Yamada K., Yu G., Yuan S., Shinozaki K., Ecker J., Theologis A.,
RA Davis R.W.;
RL Submitted (DEC-2002) to the EMBL/GenBank/DBJ databases.
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DR EMBL; BT002530; AAO00890.1; -.
KW Kinase.
SQ SEQUENCE 652 AA; 72656 MW; 705751BAAL5C4E05 CRC64;

Query Match 66.1%; Score 3316; DB 10; Length 652;
Best Local Similarity 100.0%; Pred. No. 4.9e-210;
Matches 652; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 330 MHCPRFKHLPIPWTAITPSSILVLVITFLVGYILYBAINRIATVEEDCQKRELKARAEAA 389
DB 1 MHCPRFKHLPIPWTAITPSSILVLVITFLVGYILYBAINRIATVEEDCQKRELKARAEAA 60
QY 390 DIAKSQFLATVSHIEIRTPMNGVLGMLKMLMDTDLDAKOMDYAQAHAHSGKDLTSLINEVL 449
DB 61 DIAKSQFLATVSHIEIRTPMNGVLGMLKMLMDTDLDAKOMDYAQAHAHSGKDLTSLINEVL 120
QY 450 DQAKIESGRLELENVPPDMRFILDNVSSLSGKANEKIGIELAVVSVQPDVVGDPDSRF 509
DB 121 DQAKIESGRLELENVPPDMRFILDNVSSLSGKANEKIGIELAVVSVQPDVVGDPDSRF 180
QY 510 ROIITNLVGNISIKFTQERGHIFISVHLADEVKEPLTTIEDAVLKORLALGSESEGETVSGF 569
DB 181 ROIITNLVGNISIKFTQERGHIFISVHLADEVKEPLTTIEDAVLKORLALGSESEGETVSGF 240
QY 570 PAVNANGSWKNFKTCYTESQNSDOIKLVTVEDTGVGIPVDAQGRIFTFPMQADSSTSR 629
DB 241 PAVNANGSWKNFKTCYTESQNSDOIKLVTVEDTGVGIPVDAQGRIFTFPMQADSSTSR 300
QY 630 TVGGTGIGLSISKRLVELMQEMGFVSEPGISTFTGVFGKAEATNTSITKLERFDLAI 689
DB 301 TVGGTGIGLSISKRLVELMQEMGFVSEPGISTFTGVFGKAEATNTSITKLERFDLAI 360
QY 690 Q8FTGLRALVIDNRIAEVTRVRLRLGISADIVSSLRMACTCCISKLENLAMILIDKD 749
DB 361 Q8FTGLRALVIDNRIAEVTRVRLRLGISADIVSSLRMACTCCISKLENLAMILIDKD 420
QY 750 ANKKEEFSVLDLFTRSKVTFTRPVKIFLLATSATLTERSEMSKSTGLIDEVVIKPLRMSV 809
DB 421 ANKKEEFSVLDLFTRSKVTFTRPVKIFLLATSATLTERSEMSKSTGLIDEVVIKPLRMSV 480
QY 810 LICCLQETLVNGKKRQPNRQRLNHLRLREKQILVNDNLNRRVAEGALKKYGAIVTCV 869
DB 481 LICCLQETLVNGKKRQPNRQRLNHLRLREKQILVNDNLNRRVAEGALKKYGAIVTCV 540
QY 870 ESGKAALAMKPPNFACFMDLQMPMDGFATRRVRELEREINKKIASGEVSAEMFCF 929
DB 541 ESGKAALAMKPPNFACFMDLQMPMDGFATRRVRELEREINKKIASGEVSAEMFCF 600
QY 930 FSSWHVPILAMTADVIQATHECMKCGMDGYVSKPFEEVLYTAVARFFEP 981
DB 601 FSSWHVPILAMTADVIQATHECMKCGMDGYVSKPFEEVLYTAVARFFEP 652

RESULT 4
Q8L816
ID Q8L816 PRELIMINARY; PRT; 1041 AA.
AC Q8L816;
DT 01-OCT-2002 (TrEMBLrel. 22, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Cytokinin receptor.
GN CKR1.
OS Catharanthus roseus (Rosy periwinkle) (Madagascar periwinkle).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
OC Asteridae; lamids; Gentianales; Apocynaceae; Rauvolfioideae; Vinceae;
OC Catharanthus.
OX NCBI_TaxID=4058;
RN [1]
RP SEQUENCE FROM N.A.
RA MEDLINE=22166729; PubMed=12177139;
RA Papon N., Clastre M., Andreu F., Gantet P., Rideau M., Creche J.;
RT "Expression analysis in plant and cell suspensions of CrCKR1, a cDNA
```

RT	encoding a histidine kinase receptor homologue in Catharanthus roseus
RL	(L.) G. Don."
JL	J. Exp. Bot. 53:1989-1990(2002).
DR	EMBL; AY092025; AAM14700.1; -
DR	InterPro; IPR003594; AtPbind_ATPase.
DR	InterPro; IPR004358; Bact_sens_pr.C.
DR	InterPro; IPR006189; CHASE.
DR	InterPro; IPR003661; His_kinA.
DR	InterPro; IPR005467; His_kinase.
DR	InterPro; IPR001789; Response_reg.
DR	pfam; PF03924; CHASE; 1.
DR	pfam; PF02518; HATPase.c; 1.
DR	pfam; PF00512; Hiska; 1.
DR	pfam; PF00072; response_reg; 1.
DR	PRINTS; PR00344; BCRLSENSOR.
DR	ProDom; PD000039; Response_reg; 1.
DR	SMART; SMC00387; HATPase_c; 1.
DR	SMART; SMC00388; Hiska; 1.
DR	SMART; SMC00448; REC; 1.
DR	PROSITE; PS00839; CHASE; 1.
DR	PROSITE; PS0109; HIS_KIN; 1.
DR	PROSITE; PS0110; RESPONSE_REGULATORY; 1.
KW	Phosphorylation; Receptor; Sensory transduction.
SQ	SEQUENCE 1041 AA; 116697 MW; 8A56658493C1C48 CRC64;
Query Match 65.7%; Score 3297.5; DB 10; Length 1041;	
Best Local Similarity 66.1%; Pred. No. 1.7e-208;	
Matches 656; Conservative 133; Mismatches 189; Indels 15; Gaps 5	
QY	1 KARGERKKVHLQALAPKPKQQQAQTSSRAGGRWRKNILLGILGGVSFSVWFWDNNE 60
DB	48 KQKSVEEQPLNQQLQHFFHQOIQNTSRGTGWKTLLVVFLVLAGFGSNLPWLSE 107
QY	61 EIIIMKRRETLANMCDERARVLQDQPNVSLNHVALHSILVSTFHHOKIPSAIDQRTEBYT 120
DB	108 DSKLRKETETLASMCDERARMLODQPNVSLNHVALAILVSTFYHGKEPWALDDQTFEYDT 167
QY	121 ERTNFERPLSGVAAYLVPHSEREKPEKGWAIKKMETEDOTVVOOCVENPDPAPIO 180
DB	168 EKTAFAERPLTSGVAAYLVHLSEREKFKEQGOWIIRKMDTEVTQTIGQDLVPKELSPAPVQ 227
QY	181 DEYAPVIFAQTVSHIVSDVMWSGBEDRENILRAPASGKVLTSPFKLLKSNHLGWLTFF 240
DB	228 TEYAPVIFAQTVSHIVSIDMWSGKDRENILRAPASGKVLTSPFKLLKSNHLGVLTFF 287
QY	241 AVYTSLPPDATEGEORVETATGYLGASVDMSLEVKLLHQLASKOTIAVDVTDTTNTSGL 300
DB	288 AVYNTDLPPEATREQRI NATVGYLGSYDVPSLEVKLHLQASKOTIAVNYYDTTDDKAP 347
QY	301 IKMYGSEIGDISEQHISLSDGDPGRNHEMHCRPKHKPIPMWTATPSILVLVIITFLVGY 360
DB	348 IKMTGDRAUNTGLPRI SQLDFGDPGRKHEMHCRFKQKPPPWTALLASGVGLVITILLGH 407
QY	361 ILYEAINRIATVEEDCCQMRSLKARAEEADIAKSFQATVTSHEIRTPMNGVLGMKMLMD 420
DB	408 IFHAAINRIAKVERDYREMALKHRAEAADI AKSQFLATVSHEIRT PMVGVLGMQLMLG 467
QY	421 TDLDAKMQDYAQTAGHSGKOLTSLINEVLDQAKIESGLEILENVFPDMRFILDNVSSLIS 480
DB	468 TNLVDVKQLDYAEETHASGKOLISLINEVLDQAKIESGLEILEAVPFDLRADLDKVVSSLIS 527
QY	481 GKANEKGTELAVYSSQVDPVVVGDPSPFRQIITNLVGNISKFTQERGHI FTSVHLADRV 540
DB	528 GKSHEKDELAVYSDQVPEVVGDPGRFRQIITNLVGNISKFTDKGHI FTSVHLADRV 587
QY	541 KEPLTIEDAVLKQRLAL---GCSESGEVTSVGPAPVNAWGSKWNFKTCTYSTESQNDSQIKL 597
DB	588 KSPLDKDEVLKQSLLTLQDRSTASFNLISGFPPVDRWRSWEKFN-LSGMEFEKKIKL 646
QY	598 LVTVEDTGCVIPDAQGRIFPTFMQADSTSTSYGGTGIGUISIKRLVELMGEMGCFVSE 657
DB	647 LVTVEDTDGTVYDAQDIRFTFPVQADSSTSKYGTGIGUISIKRLVDLVGEGICFVSE 706

QY	658	PGIGSTFSTGVGKGAETWTSITKLRFPLATQETGLRALVTDNENIRAEVTRVELRL	717
Db	707	PGGSGTSTFAAFTKAETITGKMEQYDLAVSEFGLKALVVDKSIIRAEVTRYQLKRL	766
QY	718	GISADITVSL-----RMACTCCISKLENLAMILIDKADWNKBEFVSVDLFTFSKVTFTFR	772
Db	767	EVSVDIATVEAAYSHLSDVNSSASERYSVMLIDSDSDNNEIMARYVVGCLKSDQASR	826
QY	773	V-----PKTFLIATSATLTERSEMKSTGLIDEVVIKPLRMSVLICLQETLVNGKKRQPN	827
Db	827	PSGMGNPKIFLLANPKPSFDCIELKSTGLVDNVLTKPLRLSILISLCIQESIGFGRQVT	886
QY	828	RQR-RNLGHLIREKQTLVVDNVLNVRVAEGALKKYCAIVTCVSGKAALAMLKPPHNF	886
Db	887	RNPSTIGNLLKGRMLVVDNPNVRKVAELARUKYGAVVTCBASGEAALQRLKPPHDF	946
QY	887	ACFMDLQMPMDGFATRVRELEREINKKIASGEVSAEMCKCFSSWHVPILAMTADVIQ	946
Db	947	ACFMDLQMPMDGFQATQKIRHLERYENNVKSGEIGTKDSTDEAYWHITLMTADLIQ	1006
QY	947	ATHECMCKMDGYVSKPFEFEVLYTAVARFFE	979
Db	1007	ATNEKCRKCGMDGYVSKPFDDEQLYSAVAPFFK	1039
RESULT 5			
Q9CSUI PRELIMINARY; PRT; 1036 AA.			
ID	Q9CSUI	AC	Q9CSUI;
DT	01-JUN-2001	(T-EMBLrel. 17, Created)	
DT	01-JUN-2001	(T-EMBLrel. 17, Last sequence update)	
DT	01-MAR-2003	(T-EMBLrel. 23, Last annotation update)	
DE	Histidine kinase.		
GN	ANK3.		
OS	Arabidopsis thaliana (Mouse-ear cress).		
OC	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;		
OC	Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;		
OC	eurosid II; Brassicales; Brassicaceae; Arabidopsids.		
NCBI_TaxId	=3702;		
RN	[1]		
RP	SEQUENCE FROM N. A.		
RX	MEDLINE=21154803; PubMed=11230578;		
RA	Ueguchi C., Kozumi H., Suzuki T., Mizuno T.;		
RT	"Novel family of sensor histidine kinase genes in Arabidopsis		
RL	thaliana.";		
RL	Plant Cell Physiol. 42:231-235(2001).		
DR	EMBL; AB046870; BAB40775.1; -		
DR	HSSP; P06143; IAB6		
DR	InterPro; IPR003594; ATPbind_ATPase.		
DR	InterPro; IPR006189; CHASE.		
DR	InterPro; IPR003661; His_kinase.		
DR	InterPro; IPR005467; His_kinase.		
DR	InterPro; IPR001789; Response_reg.		
DR	Pfam; PF03924; CHASE; 1.		
DR	Pfam; PF02518; HATPase_c; 1.		
DR	Pfam; PF00512; Hiska; 1.		
DR	Pfam; PF00072; response_reg; 1.		
DR	ProDom; PD000039; Response_reg; 1.		
DR	SMART; SM00387; HATPase_c; 1.		
DR	SMART; SM00388; Hiska; 1.		
DR	SMART; SM00448; REC; 2.		
DR	PROSITE; PS50839; CHASE; 1.		
DR	PROSITE; PS50109; HIS_KIN; 1.		
DR	PROSITE; PS50110; RESPONSE_REGULATORY; 1.		
DR	Kinase; Phosphorylation; Sensory transduction.		
SW	SEQUENCE 1036 AA; 116373 MW; 03F23DEE4B44C40B CRC64;		
Query Match 53.5%; Score 2685.5; DB 10; Length 1036;			
Best Local Similarity 57.2%; Pred. No. 3.9e-168;			
Matches 551; Conservative 142; Mismatches 224; Indels 47; Gaps 13;			
QY	35	WRKNHLLGLGVGSVWFWFDTNSEEIMKRRETLANMCDERARVLQDQFNVSLNHVHA	94

Db 92 WRK-LVVVVVVVWVLSVITWTFWFSQWAMEKKEKTELASMCDEARMLQDQFNVSNNHYQA 150
Qy 95 LSLIVSTPHHOKIPSAIDQRTPEETERTNTERPLTSGVAYALKVPHSERKPEKEHWA 154
Db 151 MSILISTPHHOKIPSAIDQRTPEETERTNTERPLTSGVAYAMRVLHSEFEFRQCGWT 210
Qy 155 IKKMETEDQTVV--QDCVPENFDPAIDVAPVIFAQETVSHIVSDVMSSGEEDRENIL 212
Db 211 IRKMSYLSQNPVHKDDYDLEALPSPQVEEYAPVIFAQDTVSHVVSLSLMSKEDRENVL 270
Qy 213 RARASGKGVLTSPFKLLKSNHGLVLTFAVYDTSLLPDPATBEQREARVIGYLGASDMP 272
Db 271 PARSSEKGVLTAPPLIKTNRLGVLTFAVYKEDLPSTATPKERLEANGVYLGVDIES 330
Qy 273 LVEKLLHOLASQTTAVDYDTNTSGLIKMYSGEIGDISQHISLSLDFGPPSRNHEMHC 332
Db 331 LVENLLOLQASKQTLVNVYDITNHSQPISTMYGTNVSDGLERVSPLIFGDLRKHMER 390
Qy 333 RPKHKLPTWTAITPSILVLTFTFVGLVLYEAINRIATVEEDCKMRELKARAAADIA 392
Db 391 RPKQPPVPLVSMVTSFGILVLTALLVAHIHATVSRHKVEEDCKMKOLKKKAADVA 450
Qy 393 KSQFLATVSHERTPMGVLMKMLMDTDLDAKQMDYAQTAAHSGSKDLTSLINEVLDOA 452
Db 451 KSQFLATVSHERTPMGVLMKMLMDTDLDTQDYVRTAAQASGKALVSLINEVLDOA 510
Qy 453 KIESGRLENNVFPMDRILNVSSLSGKANKEGIELAVYVSQVDDVGVDPSPRFQI 512
Db 511 KIESGKLEEVRFDLRGDLDVLSFSSKQKQVELAVYISDRVPMGLIGDPGRFQI 570
Qy 513 ITNLVNSIKTTOERGHIFISVHLADEVKEPTIEDAVLKQRLALGCSGETVSGFAV 572
Db 571 LTNLMGNSIKFT-EGHIFVTVHLVDELFSIDGETA-----SPSESTLSGLFVA 619
Qy 573 NAWGSKWKNFKCTYESQNS-----DQIKLLVTVEDTGVIPVDAQGRIFTPFMAQDSST 627
Db 620 DRQSWENFK-AFSSNGHRSFEPSPDNLIVSVDGTGVIPVEAQSRIFTPFMQVGS 678
Qy 628 SRTYGGTIGLISIKRLVELMGQGVSEPGIGTFTFTGVFG-----KATNTSI 679
Db 679 SRTYGGTIGLISIKRLVELMGQGVSEPGIGTFTFTGVFG-----KATNTSI 679
Qy 680 TYLERPDIAQFTGERALVDNRIRAEVTRFELRLGISADIVSSLRMACTCISKLE 739
Db 739 -----FSEFRGMKAVVDDHRRPARAKVSWYHFQRLGIRVEVVRVEQALHYLKIGTT 789
Qy 740 NLAMILIDKAWNKEFSVLDELFTSRKVTFTRVPKIFLATSATLTERSEMKSTGLIDE 799
Db 790 TVNMILIEQEIWNREDDFIKL-----QKDPLFLSPALILLANSVE-SSISEALCTG-IDP 844
Qy 800 --VVIKPLRMSYLIICLQETLVNGKKQFNRO--RRNLGHLLEKQKILVDDNLVNRV 854
Db 845 PIVIVKPLRASMLAATLQRLGIGIGIREPPQHKGPALILRNLLGKILVDDNNVLRV 904
Qy 855 AEGALKKYGAIVTVESGKAALAMLPKPHNFDACFMDLQMPMDGFEATRVRLEERIN 914
Db 905 AAGALKKYGADVCAESGKATSLKLPHEFDACFMDIQMPMDGFEATRIRDMEBEYN 964
Qy 915 KIASGEVSAEMFCKPSSWHVPIAMTADVIOATHEECMKCMDCGVSKPPEEVLVYAV 974
Db 965 KRKKGALIVENGKNSWHLPLVMTADVIOATHEECLKCMDCGVSKPPEEVLVYREV 1024
Qy 975 ARFF 978
Db 1025 SRFF 1028

RESULT 6

Q9FZK3

ID Q9FZK3

AC Q9FZK3

DT 01-MAR-2001 (TReMBLrel. 16, Created)

01-MAR-2001 (TReMBLrel. 16, Last sequence update)

DT 01-MAR-2003 (TReMBLrel. 23, Last annotation update)
DE F17L21.11;
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eucosids II; Brassicales; Brassicaceae; Arabidopsids.
OX NCBI_taxID=3702;
RN [1]
RP SEQUENCE FROM N.A.
RA Johnson-Hopson C., Brooks S., Buehler E., Chao Q., Khan S., Kim C.,
RA Shinn P., Altafi H., Bei Q., Chin C., Chioi J., Choi E., Conn L.,
RA Conway A., Gonzales A., Hansen N., Howing B., Koo T., Lam B., Lee J.,
RA Lenz C., Li J., Liu A., Liu K., Liu S., Mukharsky N., Nguyen M.,
RA Palm C., Pham P., Sakano H., Schwartz J., Southwick A., Thaverl A.,
RA Toriumi M., Vaysberg M., Yu G., Federspiel N.A., Theologis A.,
RA Ecker J.R.;
RT "Genomic sequence for Arabidopsis thaliana BAC F17L21 from chromosome
I.";
RL Submitted (APR-1998) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RA Ecker J.R.;
RL Submitted (APR-1998) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RA Ecker J.R.;
RL Submitted (JUN-1998) to the EMBL/GenBank/DBJ databases.
RN [4]
RP SEQUENCE FROM N.A.
RA Ecker J.R.;
RL Submitted (DEC-1998) to the EMBL/GenBank/DBJ databases.
RN [5]
RP SEQUENCE FROM N.A.
RA Ecker J.R.;
RL Submitted (AUG-2000) to the EMBL/GenBank/DBJ databases.
RN [6]
RP SEQUENCE FROM N.A.
RA Cheuk R., Shinn P., Brooks S., Buehler E., Chao Q., Johnson-Hopson C.,
RA Khan S., Kim C., Altafi H., Bei B., Chin C., Chioi J., Choi E.,
RA Conn L., Conway A., Gonzales A., Hansen N., Howing B., Koo T., Lam B.,
RA Lee J., Lenz C., Li J., Liu A., Liu J., Liu S., Mukharsky N.,
RA Nguyen M., Palm C., Pham P., Sakano H., Schwartz J., Southwick A.,
RA Thaverl A., Toriumi M., Vaysberg M., Yu G., Davis R., Federspiel N.,
RA Theologis A., Ecker J.;
RL Submitted (AUG-2000) to the EMBL/GenBank/DBJ databases.
RN [7]
RP SEQUENCE FROM N.A.
RA EMBL; AC004557; AAF99730.1;
DR InterPro; IPR003594; ATPbind_ATPase.
DR InterPro; IPR004358; Bact_sens_pr_C.
DR InterPro; IPR006189; CHASE.
DR InterPro; IPR003661; His_kinA.
DR InterPro; IPR005467; His_kinase.
DR InterPro; IPR001789; Response_reg.
DR Pfam; PF03924; CHASE; 1.
DR Pfam; PF02518; HATPase_c; 1.
DR Pfam; PF00512; HSKA; 1.
DR Pfam; PF00072; response_reg; 1.
DR PRINTS; PR00344; BCTRLSENSOR.
DR PRODOM; PD000039; Response_reg; 1.
DR SMART; SM00387; HATPase_c; 1.
DR SMART; SM00388; HSKA; 1.
DR SMART; SM00448; REC; 2.
DR PROSITE; PS50839; CHASE; 1.
DR PROSITE; PS50109; HIS_KIN; 1.
DR PROSITE; PS50110; RESPONSE_REGULATORY; 1.
KW Phosphorylation; Sensor; transduction.
SQ SEQUENCE 1092 AA; 122824 MW; 7250C55873A216B CRC64;

Query Match

Best Local Similarity 51.7%; Score 2595.5; DB 10; Length 1092;

Matches 538; Conservative 141; Mismatches 220; Indels 79; Gaps 14;

Qy 35 WRKNILLGILGVGSFVSFWWFWDNNEIIMKRRTLANMCDERARVLQDQFNVSINHYHA 94

01-MAR-2001 (TReMBLrel. 16, Last sequence update)

Db 92 WRK-LVVVVVFWVLVSIWTFYFSSQAMKREKETLASMCDEARMLQDFNVNMHVOA 150
QY 95 LSLIVSTFHGKIPSAIDORTTEYTERTNFERPLTSGVAYALKVPHSREKFEKEHGA 154
Db 151 MSILISTFHGKIPSAIDORTSEYTDRTSFRPLTSGVAYAMRVLSHREFEQOQWT 210
QY 155 IKKMETEDQTVV--QDCVPENFDPAIQDEYAPVIFAQTVSHVSDVMMSGEEDRENIL 212
Db 211 IRKMSLEQNPVHKDDYDLEALEPSPVQEBYAPVIFAQTVSHVSDMLSGEDRENVL 270
QY 213 RARASCKGVLTSPPKLLKSNHLGVLTFAVDYDTSIPPDATREORVEATIGYLGASVDMPS 272
Db 271 RARSSCKGVLTAFFPLIKTNRLGVLTFAVYKEDLPESNATPKERIBATNGYLGGVFEDIS 330
QY 273 LVEKLHLQALASKOTIAVDVYDTNTSGLIKMYGSEIGDISEQHSISLDGDPDSRNHEMH- 331
Db 331 LVENILLOALASKOTILNVYDITNHSQPSWYGTNSADGLERSVPLIFGDPPLKHEMRC 390
QY 332 -----CRFKHKLPIPWTAITPSSILVLVITVLGY 360
Db 391 RYLQLAHTVVCNFFLFARIQVLTFCCELLPLCRFKQKPPWPVLSMVTSPGILVIALLVAH 450
QY 361 ILYEAINRATVEEDCKKRELKARABADIASKQFLATVSHIRTPMNGVLNKLQMLMD 420
Db 451 ITHATVSRTHKVEEDCDKMKQKKAADAVAKSQFLATVSHIRTPMNGVLNKLQMLMD 510
QY 421 TOLDKQMDYAQTAHSGKDLTSLINEVLDQAKIESGRLELENVPPDMRPFILDNVSSILS 480
Db 511 TELDVTOQDYVTPAQASGKALVSLINEVLDQAKIESGKULEBEVRFDLGLDDVLSLPS 570
QY 481 KANEXGIELAVYVSSQVDPVVDPSRFRQIITNLVGNISIKFTQERGHIFISVHLADEV 540
Db 571 SKSQCKGVELAVISDRVPDMLGDPGRFRQIITNLVGNISIKFT-EKGHLFVTVHLVDEL 629
QY 541 KEPLTTIEDAVLKORLALGSESEGETVSGPANNAGSWKNFKTCYCTESQNS-----DQI 595
Db 630 FESIDGETA-----SSPESTLSGLPVDADRQRSWENFK-AFSSNGHRSEFPSPDI 678
QY 596 KILAVTVEDTGVPIDVDAQRIFFPFOADSTSTRTYGGTGIGLSISKRLVELMOGSMGFV 655
Db 679 NLIVSVEDTGVPIDVDAQRIFFPFOVGPISRTHTGGTGIGLSISKCLVGLMKGIGFS 738
QY 656 SEPGIGSTSFSTGVFG-----KAEITNTSITKLERFDLAIQFTGLRALVIDNRNIRA 707
Db 739 STEKVGSTFTTAVFNSGMQPAERKNDNQPI-----PSEFRGMKAVVVDHHPARA 789
QY 708 EVTRYELRLGIGSADIIVSSIRMACTCCI SKLENLAMILDKDANKKEEVSVDLEFTRSK 767
Db 790 KVSWYHFORLIGIRVEVVPVRYEQALHYLKIGTTTTVNMILLIEQETWNEADDFIKKL---QK 846
QY 768 VTETRPKIFLLATSATLTERSEMSKSLIDE--VVIKPLRMSVLICCLQETLVNGKKRQ 825
Db 847 DPLFLSPKILLANSVE--SSISALCTG-IDPPIVIVKPLRASMLAATLQRGIGIGIREP 904
QY 826 PNRQ---RRNLGHLIREKQILVVDNLVNRVRAEGALKKYGAIVTCVESKAALAMLKXP 882
Db 905 PQHKGPPALILNLLGRKILIVDDNNVNLVRAAGALKKYGADVCAESGKAIKLSLXPP 964
QY 883 HNFDAFMDLQMPMDGFEATRRLRELEREINKKIAGSEVSAEMFKFSSWHVPIILAMTA 942
Db 965 HEFDACFMDIQMPMDGFEATRIRDMEEEMNRKIKNGEALIVENGKTSWHLPVILAMTA 1024
QY 943 DVIQATHEECMKCMGMDGY 960
Db 1025 DVIQATHEECMKCMGMDGY 1042

RESULT 7

Q8RYG4

ID Q8RYG4 PRELIMINARY; PRT: 1023 AA.

AC Q8RYG4

DT 01-JUN-2002 (TREMBlrel. 21, Created)

DT 01-JUN-2002 (TREMBlrel. 21, Last sequence update)

DT 01-WAR-2003 (TREMBlrel. 23, Last annotation update)
DE Putative histidine kinase.
GN P0592G05.13.
OS Oryza sativa (japonica cultivar-group).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC Ehrhartoideae; Oryzaceae; Oryza.
OX NCBI_TaxID=39947;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=cv. Nipponbare;
RA Sasaki T., Matsumoto T., Yamamoto K.;
RT "Oryza sativa (japonica cultivar-group) genomic DNA, chromosome 1, PAC
clone:P0592G05.";
RL Submitted (JAN-2002) to the EMBL/GenBank/DBJ databases.
EMBL; AP004672; BAB90827.1; -;
DR Granene; Q8RYG4; -;
DR InterPro; IPR003594; ATPbind_ATPase.
DR InterPro; IPR006189; CHASE.
DR InterPro; IPR003661; His_kinA.
DR InterPro; IPR005467; His_kinase.
DR InterPro; IPR001789; Response_reg.
DR Pfam; PF03924; CHASE; 1.
DR Pfam; PF02518; HATPase_C; 1.
DR Pfam; PF00512; HSKA; 1.
DR Pfam; PF00072; response_reg; 1.
DR ProDom; PD000039; Response_reg; 1.
DR SMART; SM00387; HATPase_c; 1.
DR SMART; SM00388; HSKA; 1.
DR SMART; SM00448; REC; 1.
DR PROSITE; PS50839; CHASE; 1.
DR PROSITE; PS50109; His_KIN; 1.
DR PROSITE; PS50110; RESPONSE_REGULATORY; 1.
KW Kinase; Phosphorylation; Sensory transduction.
SQ SEQUENCE 1023 AA; 113219 MW; 469AC35146CDF62B CRC64;

Query Match 51.3%; Score 2575; DB 10; Length 1023;

Best Local Similarity 54.7%; Pred. No. 7.3e-161;

Matches 545; Conservative 136; Mismatches 251; Indels 64; Gaps 18;

QY 18 PKQOQRAQTSRGA-----GWRKN-----ILLILGILGVSFVSFWFNDNEELMKR 66

Db 52 PEKVSARARV-VRGSILVAHFRQWRYVRETVMWVLLWLLILAGLSGFLFLFMAQSLDKR 110

QY 67 RETLANMCDERARVLQDFNVSLNHVHALSIIVSTFHHGKIPIAIDORTFEYVTRTNE 126

Db 111 RSLASMCDEARARMLQDFNVSMNHLQALAILVSTFHHGKIPIAIDORTFEYVTRTNE 170

QY 127 RLPTSGVAYALVPHSREKFEKEHGAIKKMETEDQTVVQDCVPENFDPAIQ-----D 181

Db 171 RLPTSGVAYAVRVTHGREQERQOCQWAIKKMYSSNNKQSSPGPGDAVAEIREPAE 230

QY 182 EYAPVIFAQETVSHIVSDVMMSGEDRENILRARASCKGVLTSPPKLLKSNHLGVLTFA 241

Db 231 EYAPVIFAQDAYKHVISFDMLSGNEDRONILRARKSGKVLTAFFPKLL--NNELGVLTAT 289

QY 242 VYDTSLPDPADEORVEATIGYLGASVDMPSLVEKLLHOLASKOTIAVDVYDTNTSGLI 301

Db 290 VTKYELPAYARHERIQAAIGYLGIGIFDIQALVEKLLQKLAQSESIMNVYDITNESP-I 348

QY 302 KMYGSEIGDISQHSISLDFGDPDSRNHEMHCHFKHLPIPWTAITPSSILVLVITVLGYI 361

Db 349 SMYGGDTGS-GMCHSVSLNFGDPSPRKHMHCHCFEKPPWPWLAITSSFGTLVIALLTGHI 407

QY 362 LYEAINRATVEEDCKKRELKARABADIASKQFLATVSHIRTPMNGVLNKLQMLMDT 421

Db 408 FOATVHTIAKVEDDFHKMSSELKKRAEDADVAKSQFLATVSHIRTPMNGVLNKLQMLMDT 467

QY 422 DLDKQMDYAQTAHSGKDLTSLINEVLDQAKIESGRLELENVPPDMRPFILDNVSSILS 481

Db 468 DLDTTQDDYVTPAQASGKALVSLINEVLDQAKIESGKULEBEVTPFDLRTVCCDDILSLFCG 527

QY 482 KANEXGIELAVYVSSQVDPVVDPSRFRQIITNLVGNISIKFTQERGHIFISVHLADEVK 541


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QY 931 SSWHVPILAMTADVIQATHEECMKCMGCVGSKPFEVEVLYTAVARFEP 980
DB 1001 LEWHLPIAMTADVIHATYEECLKSGMDGVGSKPFEENLYKSAKSPK 1050

RESULT 9
Q9C5T8 PRELIMINARY; PRT; 1080 AA.
ID Q9C5T8 PRELIMINARY; PRT; 1080 AA.
AC Q9C5T8;
DT 01-JUN-2001 (Tremblrel. 17, Created)
DT 01-JUN-2001 (Tremblrel. 17, Last sequence update)
DT 01-MAR-2003 (Tremblrel. 23, Last annotation update)
DE Cytokinin receptor CRE1b.
GN CRE1.
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eurosids II; Brassicales; Brassicaceae; Arabidopsis.
OX NCBI_TaxID=3702;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=cv. Wassilewskija;
RA Inoue T., Higuchi M., Hashimoto Y., Seki M., Kobayashi M., Kato T.,
RA Satoshi T., Shinozaki K., Kakimoto T.;
RT "Identification of a cytokinin receptor, CRE1, from Arabidopsis.";
RL Submitted (OCT-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AB049935; BAB33311.1; -.
DR HSSP; P06657; 2CHF.
DR InterPro; IPR003594; ATPbind_ATPase.
DR InterPro; IPR004358; Bact_sens_pr_C.
DR InterPro; IPR006189; CHASE.
DR InterPro; IPR003661; His_kinA.
DR InterPro; IPR005467; His_kinase.
DR InterPro; IPR001789; Response_reg.
DR Pfam; PF03924; CHASE; 1.
DR Pfam; PF02518; HATPase; 1.
DR Pfam; PF00512; Hiska; 1.
DR PRINTS; PF00072; response_reg; 1.
DR ProDom; PD000039; Response_reg; 1.
DR SMART; SM00387; HATPase_C; 1.
DR SMART; SM00388; Hiska; 1.
DR SMART; SM00448; REC; 1.
DR PROSITE; PS00839; CHASE; 1.
DR PROSITE; PS0109; HIS_KIN; 1.
DR PROSITE; PS0110; RESPONSE_REGULATORY; 1.
KW Phosphorylation; Receptor; Sensory transduction.
SQ SEQUENCE 1080 AA; 120670 MW; 59496F734B528114 CRC64;

Query Match 50.7%; Score 2545.5; DB 10; Length 1080;
Best Local Similarity 53.3%; Pred. No. 7.le-159;
Matches 538; Conservative 152; Mismatches 239; Indels 81; Gaps 17;

QY 4 GERKEVHLQE--ALAPKKQQRAQTSRRGAGRWKRNILLGLGCVSFVW-WFMDTNE 60
DB 112 GNKKGSTFQEHALPLKAL-----ILWIIIVGSIQWMDANK 154

QY 61 EIMKRETLANCDERARVLPQFNVLNHNHVALSILVSTFHGKIPSAIDQRTPEYV 120
DB 155 ---IRREEVLVSCDQRMQLQDFSVNVHVALAILVSTFHYHKNPSAIDQETFAEYV 211

QY 121 ERTNPERPLTSGVAYALKVPHSEREKEFEHGWAIKKMETEDQTVVQDCVPENFDPAPIQ 180
DB 212 ARTAFERPLSGVAYAEKVNVFERNFERQHNVIKTM-----DRGEFSPVR 258

QY 181 DEYAVIPFAQETVSHLVSDMMSGEEDRENILPARASGKVLTPSPKLLKSNHLGVVLPF 240
DB 259 DEYAVIPFQDSVSYLSLSDMMSGEEDRENILPARGTGKAVLTSPFLLETHLGVVLPF 318

QY 241 AVYDTSLPDPATBEQVEATIGYLGASDYMPSLVEXLLHQLASKQTIADVVDYDTNTSG 300
DB 319 PVYKSLPENPTVVEERIAATAGYLGAFDVSILVENLLGQAGNQAIVVHVYDITNASDP 378
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QY 301 IKMYS--EIGDISQHILSLDFGDPSSNHEHCRFKHKLPIPWTAITPSILVLVITLV 358
DB 379 LVMYQNQDEEADRSLSHESKLDGDFPKHKMKIKNYHOKAPILPNVLVITVFLFFAIGFLV 438

QY 359 GYILYEAINRIATVEEDCQKRELKARAAADIAKQSFATVSHIRTPMNGVLGMLKML 418
DB 439 GYILYGAAMHIVKVEDDFHEMOELKVRAEADVAKSQFLATVSHIRTPMNGILGMLAML 498

QY 419 MDTDLDAKQMOYQAOTAHSGKDLTSLINEVLDOAKIESGRLELENVPPFMDRFLDNVSSL 478
DB 499 LDTELSSTQRDYAQTAAQVCGKALIALINEVLDRAKIEAGKLELSVPEDIRSLDDVLSL 558

QY 479 LSGKANEGIELAVVSSQVDPVVVGDPSRQIITNLVGNISIKETQERGHIFISHLAD 538
DB 559 FSESRNKGIELAVPVSKVFEIVKDGSRFQIILNLVGNVSKET-EGKHIFVVKHIAE 617

QY 539 EVK---EPL-TIEDAVLKQRIALGCESETVSGPAPVNAWGSKNFKTICYSTESQSD- 593
DB 618 QSKDESEPKNALGGVSEMIWVSKQSYNTLSGYEAAADGRNSWDSFKHLVSEEQSLSEF 677

QY 594 ----QIKLLVTVEDTCVGPVDAQGRIFTFPMQADSSSTRYGGTGIGLISIKRLVELMQ 649
DB 678 DISSNVRLMWSTEDTGIGIPLVAQGRVPMFPMQADSSSTRYGGTGIGLISIKCLVELMR 737

QY 650 GEMGVSEPGIGSTPFTGVEGKATNTSITKLER--FDLAIQEFGLRALVIDNRNIRA 707
DB 738 GQINFISRPHGISTFWFTAVLEKDCSAINHMKAPNVEHLPTSTFKGMALVVDKAPRA 797

QY 708 EYTRYELRLGISADIVSSLRMACTCCISKLEN-----LAMILDKDAW-----NK 753
DB 798 AVTRYHMKRLGINVDVVTSLKTAVAAAFERNQSGSLPTKPLQDMLIVEKDSWISTEDND 857

QY 754 BEPSVLDELFTRSKVTFTTRVPKIFLLATSAILTERSENKSTGLIDEVWIKPLRMSVLCC 813
DB 858 SEIRLLNSR-TNGNV-HHKSPKALFATNITNSEFDRAKSAGFADVTMKPLRASMIGAC 915

QY 814 LQETLVNGCKQPNRQREN--LGHLLREKQILVVDDNLVNRVRAEGALKKYGAIVTCVE 870
DB 916 LQQVLELRTKQHPGEGSPATLKSLTGKILVDDNLVNRVRAAGALKKFGAEVVCAB 975

QY 871 SGKAALAMLKPPHNFDFACFMDIQEMDGFATRRVRELEREINKKIASGEVSAEMFCFK 930
DB 976 SGQVALGLLQIPHTEFDFACFMDIQMDGFATRQIRMKEAKEKTN-----1023

QY 931 SSWHVPILAMTADVIQATHEECMKCMGCVGSKPFEVEVLYTAVARFEP 980
DB 1024 LEWHLPIAMTADVIHATYEECLKSGMDGVGSKPFEENLYKSAKSPK 1073

RESULT 10
Q9SIT0 PRELIMINARY; PRT; 1057 AA.
AC Q9SIT0; Q9FD23;
DT 01-MAY-2000 (Tremblrel. 13, Created)
DT 01-JUN-2002 (Tremblrel. 21, Last sequence update)
DT 01-MAR-2003 (Tremblrel. 23, Last annotation update)
DE Putative histidine kinase (Putative histidine kinase receptor).
GN AT2G01830 OR WOL.
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eurosids II; Brassicales; Brassicaceae; Arabidopsis.
OX NCBI_TaxID=3702;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=cv. Columbia;
RA Lin X., Kaul S., Shea T.P., Fujii C.Y., Shen M., VanAken S.E.,
RA Barnstead M.E., Mason T.M., Bowman C.I., Renning C.M., Benito M.-I.,
RA Carrera A.J., Creasy T.H., Buell C.R., Town C.D., Nierman W.C.,
RA Fraser C.M., Venter J.C.;
RL Submitted (FEB-2002) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
```


SEQ	SEQUENCE	1080 AA; 120730 MW; 5950DB968B529401 CRC64;
Query Match	50.8%; Score 2539.5; DB 10; Length 1080;	
Best Local Similarity	53.2%; Pred. No. 1.8e-158;	
Matches	537; Conservative 152; Mismatches 240; Indels 81; Gaps 17;	
QY	4 GERKEVHLQE--ALAPKKQQQAQTSRRGAGRWKKNILLGLTGVGSFVW-WFWDYNE 60	
Db	112 GNKGSTTFQEHALLPKAL-----ILWIVGSISSGIWQMDANK 154	
QY	61 EIIMKRETLANCDERARVLQDFNVSLNHVHALSILVSTFHGKIPSAIDQRTFEYT 120	
Db	155 ---IRREELVNSMCDQARMLQDFSVYNHVHALVSTFHYHKNPALDQETFAET 211	
QY	121 ERTNFRPLTSGVAYALKVPHSREKPEKHEGWAIKKMETEDQTVVQDCVPENFDPAIQ 180	
Db	212 ARTAFERPLLSGVAYAEKVNVFEREMFERQHNWIKTM-----DRGESPVR 258	
QY	181 DEYAPVIFAQETVSHIVSDVMMSGEEDRENILRARASGKGLTSPEKLLKSNHGLGVLT 240	
Db	259 DEYAPVIFQDSVSYLESIDMMSGEEDRENILRARETGKAVLTSPRLLETHHGLGVLT 318	
QY	241 AVYDTSLPDATEEQRVEATIGYLASDYMPSLVEKLLHQLASKQTIADVVDYDNTNSSL 300	
Db	319 PVYKSLPENPTVEERIAATAGYLGADFVESLVENLGLAGNQAI VVVVDYDINASDP 378	
QY	301 IKMYS--EIGLISEQHISSLDFGDSRNMHCPRFKHKLPIPWTAITPSIIVLVTPLV 358	
Db	379 LVMYGNQDEADRSLSHESKLPFGDPFRKHMICRYHQKAPILPNLVLTVPVFAIGTLV 438	
QY	359 GYLVEAINRIATVEDCOKRELKARAAADIAKSQFIATVSHIERTPMNGVLGMLKWL 418	
Db	439 GYLIVGAAMHIVKVEDDFHEMQLKVRAAADVAKSQFIATVSHIERTPMNGVLGMLAM 498	
QY	419 MDTDLDAKMDYAQTAGHSGKDLTSLINEVLQAKIESGRLELENVFPDMRFTILDNVSSL 478	
Db	499 LDTLSSTQDYAQTAAQVCGKALIALINEVLDRAKIEAGKLELESVPFDIRSLDDVLSL 558	
QY	479 LSGKANKEGIELAVYSSQVDDVWGDPRFRQIITNLVNSIKFTQERGHIFISVHLAD 538	
Db	559 FSEESRNSKIELAVFSDVKVPEIKVDSGRFRQIITNLVNSYKFT-ERKGI FVKVHLAE 617	
QY	539 EVK---EPL-TTEDAVLKORLALGCSEGETVSGRPVNAVWSKNKFTCYTESQNSD- 593	
Db	618 QSKDSEPKNALGVSEMI VVSKQSYNTLSGYEADGRNSWOSFHLVSEROSLSF 677	
QY	594 ----QIKLLVTVEDTGVPDQAQGRIFTFPFQADSTSTRTYCGTGIGLSIKRVLMLQ 649	
Db	678 DISSNVRLMVSIEDTGIGPLVAQGRVFPFQADSTSTRTYCGTGIGLSIKCLVELMR 737	
QY	650 GEMGFVSEPGIGSTSFVGFKAETNTSITKLER--FDLAIQBFGLRALVIDNRNTRA 707	
Db	738 GQINFISREPHIGSTFWFTAVLEKCDKCSAINMKFNVEHLPSTFKGMKAI VVDAPVRA 797	
QY	708 EVTRVELRLGTSADIVSSLRMACTCCISKLEN-----LAMLLIDKDAW----NK 753	
Db	798 ATRHYMKELGINVDVVTSEIKTAVVAAAAPENGSPLPKPDMLLVSKOSWISTEDND 857	
QY	754 BEFVSLDELFTRSKVTFTRVPKIFLLATSATLTERSEMKSSTGLIDEVVIKPLRMSVLICC 813	
Db	858 SEIRLINSR-TNGNV-HHKSPLALFATNITNSEFDRKSAAGFADIVIMKPLRSMIGAC 915	
QY	814 LQETLVNGKKRQNRGRN---LGHLLREKQILVDDNLVNRVRVAGALKKYGAIVTCVE 870	
Db	916 LOQVLELRTRQHPGESSPATLKSLLTGKILVDDNINVRVRVAGALKKFGAEVVCAC 975	
QY	871 SGKAALAMLKPPHNFACFMDLQMPMDGFEATRVRLELERINKKIASGEVSAEMFCF 930	
Db	976 SQGVALLGLQIPHTFDACFMDLQMPMDGFEATRQIRMMKEKTEKTN-----1023	
QY	931 SSWHPILAMTADVIQATHEECMKCGMDGYVSKPFEVEEVLVYTAVARFFEP 980	
Db	1024 LEWHLPIAMTADVIHATVEECLKSGMDGYVSKPFEENLYKSAKFKP 1073	

RESULT 12

Q8S6P5

ID	Q8SGP5	PRELIMINARY;	PRT;	925 AA.
AC	Q8SGP5;			
DT	01-JUN-2002 (TREMELrel. 21, Created)			
DT	01-JUN-2002 (TREMELrel. 21, Last sequence update)			
DT	01-MAR-2003 (TREMELrel. 23, Last annotation update)			
DE	Putative histidine kinase.			
GN	OSJNBA0073L01.1.			
OS	Oryza sativa (japonica cultivar-group).			
OC	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;			
OC	Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;			
OC	Ehrhartoideae; Oryzeae; Oryza.			
OX	NCBI TaxID=39947;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RC	STRAIN=cv. Nipponbare;			
RA	Buell C.R., Yuan Q., Ouyang S., Liu J., Gansberger K., Kim M.M.,			
RA	Overton II L.L., Bera J.J., Taitrin T., Krol M.I., Jarrahi B.B.,			
RA	Jin S.S., Koo H., Zismann V., Hsiac J., Blunt S., Vanaken S.S.,			
RA	Utterback T.T., Feldblyum T.V., Yang Q.Q., Haas B.J., Suh B.B.,			
RA	Peterson J.J., Quackenbush J., White O., Salzberg S.L., Fraser, C.M.;			
RT	"Oryza sativa chromosome 10 BAC OSJNBA0073L01 genomic sequence."			
RL	Submitted (APR-2002) to the EMBL/GenBank/DBJ databases.			
DR	EMBL; AC092548; AAM18726.1; -.			
DR	Gramene; Q8SGP5; -.			
DR	InterPro; IPR003594; ATPbind_ATPase.			
DR	InterPro; IPR006189; CHASE.			
DR	InterPro; IPR003661; His_kinA.			
DR	InterPro; IPR005467; His_kinase.			
DR	InterPro; IPR001789; Response_reg.			
DR	Pfam; PF03924; CHASE; 1.			
DR	Pfam; PF02518; HATPase_c; 1.			
DR	Pfam; PF00512; Hiska; 1.			
DR	Pfam; PF00072; response_reg; 1.			
DR	ProDom; PD00039; Response_reg; 1.			
DR	SMART; SM00387; HATPase_c; 1.			
DR	SMART; SM00388; Hiska; 1.			
DR	SMART; SM00448; REC; 1.			
DR	PROSITE; PS50839; CHASE; 1.			
DR	PROSITE; PS50109; HIS_KIN; 1.			
DR	PROSITE; PS50110; RESPONSE_REGULATORY; 2.			
KW	Kinase; phosphorylation; Sensory transduction.			
SQ	SEQUENCE 925 AA; 102928 MW; 6046D9AC28824219 CRC64;			
Query Match	50.2%; Score 2520; DB 10; Length 925;			
Best Local Similarity	59.5%; Pred. No. 2.6e-157;			
Matches	520; Conservative 116; Mismatches 216; Indels 22; Gaps 9;			
QY	61 EIIMKRETLANCDERARVLQDFNVSLNHVHALSILVSTFHGKIPSAIDQRTFEYT 120			
Db	4 DVAAERLENLNCWCDERARMLQDFNVSMNVHVALILVSTFHGKNPSAIDQKTFEFT 63			
QY	121 ERTNFRPLTSGVAYALKVPHSREKPEKHEGWAIKKMETEDQTVVQDCVPENFDPAIQ 180			
Db	64 ARTTFERLMSGVAYALKVHLHSERELFQKLGWIKKMETEDQSLVHDYNEPKLQSPVQ 123			
QY	181 DEYAPVIFAQETVSHIVSDVMMSGEEDRENILRARASGKGLTSPEKLLKSNHGLVLT 240			
Db	124 DEYAPVIFSQETVXKHISVDMMSKEDKDNILRATGKAGLTAPFPPLKSNHGLVLT 183			
QY	241 AVYDTSLPDATEEQRVEATIGYLASDYMPSLVEKLLHQLASKQTIADVVDYDNTNSSL 300			
Db	184 TVYKYDLPDPATPEERIEATIGYLGASDPVSLVERLLEQLASKQIKVIRYDITNHTYP 243			
QY	301 IKMYSGETGDISQHISSLDFGDSRNMHCPRFKHKLPIPWTAITPSIIVLVTFLVGY 360			
Db	244 TKMYDSDDVIASDDLHISNIDFGDPTRKHMVHCRFKHAPSLPWSAIMISSAVAILLVGY 303			
QY	361 ILYEAINRIATVEDCOKRELKARAAADIAKSQFIATVSHIERTPMNGVLGMLKMLMD 420			

Db 304 IIVATLSLEAEADNYTMRDLKRAEAAADVAKQFLATVSGHEIRTPMNGVLQMLQMD 363
Qy 421 TDLDAKQMDYAQTAGSGKDLTSLINEVLDQAKIESGRLELENYFPDMRFILDNVSVLS 480
Db 364 TELDTQDFVVTVAQESGKSLININEVLDLAKIESGKIELEAVRFVDRLDNVSVLS 423
Qy 481 GKANEKIELEAVVYSQVDDVVDGDPSPFROIITNLVGNISIKFTQERGHIFISVHLADEV 540
Db 424 EKSWAKGIELEAVVSDQVDFVLIGDPMRFROIITNLVGNISIKFTQERGHIFIRVHLIEV 482
Qy 541 KEPITIEDAVLKQRLAKCSBSG---ETVSGFPVAVNAGSWKNFKTCYSTESQSDQIK 596
Db 483 KRKEALDDTSPENIEVTANSKNTMPYNTLSGLEVANNRKLTESFR-MFKDSSDAIDSVN 541
Qy 597 LLVTVEDTGVGIPVDAAQGRITFPFMAQDSSTRTYGGTGIGLSISKRLVELMQEMGFVS 656
Db 542 LLVTVEDTGITTKDAQTRITFPFMAQDGSSTRTYGGTGIGLSITKRLVELMGGEIGFVS 601
Qy 657 EPGIGSTPFTGVGKAEATNTSITKLEPDLAIQEFGLRALVLDNRNIRAEVTRYELRR 716
Db 602 KPGVSTPFTSFTAIKFNKRKDPGDIKRYCPEPTFPDFQGMRALVVDGRCARAEVTRYELRR 661
Qy 717 LGISADIVSSLRMAC----TCCISKLENLAMILIDKDAWNKE---FSLVDELFTRESK 767
Db 562 LGIOCDLAATSEALSALLESCNSVKSLSNMLVDKEAWGEDSGLAFPRCLIDRLKGT 721
Qy 768 V-TFTRVPKIFLLATSAFLTERSEMKSTGLIDEVVIKPLRMSVLICCLQETLVNGKKRQP 826
Db 722 LKSMQTPKFPFLAGSITPADSDCLRLAGYNS-IRKPLRLSTVAACLSKAL--GVGLTG 778
Qy 827 NRQRN---LGHLLREKQILVVDNVLNRRVAEGALKYGAIVTCVBSGKAALAMLPHP 883
Db 779 RRSNDLSVLRSVLTGKNILVVDNNAVRIVAAAGALKYGAIVTCVDSGKAISRLQPPH 838
Qy 884 NFDACFMDLOMPMDGPEATRRVRELEIREINKKI 917
Db 839 KFDACFMDVQMPMDGPEATRLVRSVESKINDTI 872

RESULT 13
Q9FRY7 PRELIMINARY; PRT; 974 AA.
ID Q9FRY7
AC Q9FRY7
DT 01-MAR-2001 (TrEMBLrel. 16, Created)
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Histidine kinase 1.
GN ZMKH1
OS Zea mays (Maize)
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC PACCAD clade; Panicoideae; Andropogoneae; Zea.
OX NCBI_TaxID=4577;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=cv. Golden Cross Bantam T51;
RA Sakakibara H., Sugiyama T.;
RT "Cloning and characterization of maize response regulators."
RL Submitted (APR-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AB042270; BAB20583.1; --
DR HSSP; P06143; IAB6.
DR InterPro; IPR003594; ATPbind_ATPase.
DR InterPro; IPR004358; Bact_sens_pr_C.
DR InterPro; IPR006189; CHASE.
DR InterPro; IPR003661; His_kinA.
DR InterPro; IPR005467; His_kinase.
DR InterPro; IPR001789; Response_reg.
DR Pfam; PF03924; CHASE; 1.
DR Pfam; PF02518; HATPase_C; 1.
DR Pfam; PF00512; Hiska; 1.
DR Pfam; PF00072; response_reg; 1.
DR PRINTS; PR00344; BCTRLSENSOR.
DR ProDom; PD000039; Response_reg; 1.

DR SMART; SM00387; HATPase_c; 1.
DR SMART; SM00388; Hiska; 1.
DR SMART; SM00448; REC; 1.
DR PROSITE; PS00839; CHASE; 1.
DR PROSITE; PS01019; HIS_KIN; 1.
DR PROSITE; PS01110; RESPONSE_REGULATORY; 1.
KW Kinase; Phosphorylation; Sensory transduction.
SQ SEQUENCE 974 AA; 108074 MW; 3EF67B020D839F0 CRC64;

Query Match 47.1%; Score 2363; DB 10; Length 974;
Best Local Similarity 50.8%; Pred. No. 6.5e-147;
Matches 503; Conservative 152; Mismatches 251; Indels 84; Gaps 18;

Qy 34 RWRKNILLG-ILGGVSFSVWFWDTNNEEIMKRRRETLANCMDERARVLQDQFNVSLNHV 92
Db 12 RWRGLAAAGWLTAVVCSAVMHWTLRRDSMDRAEERLVSNCERARMLEQEGVTVNVH 71
Qy 93 HALSILVSTHHGKIPSAIDORTFEETERTNERPLTSGVAYALKVPHPEREKFEHGH 152
Db 72 HAITAILSTNFKEKSPPAIDQDTFAKTARTSPERPLNGVAFQAQVFFHHERMFESQQ 131
Qy 153 WAIKKMETEDQTVVQDCVPENFPAPIQDEYAPVIFAQETVSHIVSDMMSGEDRNIL 212
Db 132 WYNTMQRE-----PAPQVEYAPVIFSQDTVSYLARIDMMSGEDRNIP 177
Qy 213 PARASGKVLTSPPKLLKSNHGLVLTFAVYDTSLPPDATEEQREVEATIGYGASVDMPS 272
Db 178 RARTTGKAVLTNPFRLGSLNHLGVLTFAVVRPDLPADASVEQREVEATIGVIGGAFDVS 237
Qy 273 LVEKLLHQLASKQTIADVDDTNTSLIKMYGSEIGDISEQ-----HISLSDPDPNRH 328
Db 238 LVENLLSKLAGNQDIVVNVYDVNTNASDAMVLYGP--SSLDEQVFFLHVSLDFDGPFRKH 295
Qy 329 EMHCRFKHKLPIPTWTAITPSILVLVITFLVGYILYEAINRIATVEEDCCMKELKARAA 388
Db 296 EMCRVYKQLPMPWSAITNPLGTFIWMLLGYSTAAAYSRYDKVTECDKRWELKTQAEA 355
Qy 389 ADIAKSQFLATVSGHEIRTPMNGVLGMLKMLMDTDLDAKQMDYAQTARHSGKDLTSLNEV 448
Db 356 ADVAKSQFLATASHEIRTPMNGVLGMLDMLGTDLTMTQDYAQTACQMGCRALLTLNDV 415
Qy 449 LDQAKIESGRLELENYFPDMRFILDNVSVLSKANEKIELEAVVYSQVDDVVDGDPSPR 508
Db 416 LDRAKIEAGKLELEAVFPDLRLSMDVDVSLFSSKREKCIELAVFVCDNVPKVIGDPWR 475
Qy 509 FROIITNLVGNISIKFTQERGHIFISVHLADEVKEPLTIEDAVLKQRLAKCSBSG--- 564
Db 476 FROIITNLVGNNAVKFT-ERGHVFRVCLA-----ENSNMEANQVLHGAMNGKGRV 525
Qy 565 -----TVSGFPVAVNAGSWKNFKTCYS-----TESQN-----SDQIKLLVTV 602
Db 526 ESTANGAFNTLSGFEAADRNSNQYFKLLSDKESLDDLESENQNSQSDRVTLAISIE 585
Qy 603 DTGVGIPVDAQGRITFPFMAQDSSTRTYGGTGIGLSISKRLVELMQEMGFVSPEIGS 662
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Qy 663 TFSGTGVGKAEATNTSITKLERFDLAI-QEFTGLRALVLDNRNIRAEVTRYELRLGISA 721
Db 646 TTFSATLKSHKDIISGDSRSRITTEALPTAFKWKAILVDGRPVRSATVTHLKRGLILL 705
Qy 722 DIVSSLRMACTC-----CISKLENLAMILIDKDAWNKE-EFVSVDLDELFTRSKVTFRVP 774
Db 706 QVYNNNNAVVKAFPGQNGAAGSREKASILFIESDFWRPETDVLQNLHRLKQNGQLSDGH 765
Qy 775 KIFLLATSAFLTERSEMKSTGLIDEVVIKPLRMSVLICCLQETLVNGKKRQPNRQRN- 832
Db 766 KVVLLVTS-----EADKDKYGSIFDIVMCKPIRASTIASITQOLLKVEIAERKDNQNPFS 821
Qy 833 LGHLLREKQILVVDNVLNRRVAEGALKYGAIVTCVBSGKAALAMLPHPNHDACFMDL 892
Db 822 LRSLLVGKNILVVDNKNVLURVAAALKKYGANVSVESGKDAISLLQPPHPRFDACFMDV 881

Db 898 ELAVSEAHFKALFOGATIGV--NVDIKGLILDNQCEDMGIS---RDELRSTPIFDV 952

Qy 304 YGSBIGDISEQHISSLDPGDPSSRNHEMCRFKKLP--WTAITPSILVLVITFLV 358

Db 953 LSAQDKVAKAQFKELVGKID----HYGERSFVRPSGEPPLWVNVNSTLL-----1000

Qy 359 GYIYEAIRNRIATVEEDCQKRELKA-----RAEAADIAKSOFPLATVSHIETPM 408

Db 1001 ----DSQNFESAIVSVMDTELKLLSDELLVAKDEADAASKAKGDFLANNMHEIRTPM 1055

Qy 409 NGVLGMLKMLMDTDLDAQMDYAQTAHSGDKLJLSLINEVLDOAKIBSGRLELENVPDM 468

Db 1056 NAITGMSQLCQOTQDLDFKQKNYKIERASQSLSIINDILDFSKIBAGLDIENVSPQL 1115

Qy 469 RFILDNSSLGSKANEKGIELAVVSSQVDPVVVGGPSRFRQIITNLVGNISIKFTQBERG 528

Db 1116 DTMLEDLSDMFSERAAQOIELLPAVAPNVPRLHLLGDLPLRGVLINLMNNAIKFT-ERG 1174

Qy 529 HIFISVHLADEVKEPLTIEDAVLKORLALGSESGEIVSGPPAVNMGWKNFKTCYSTE 588

Db 1175 EVLSLSLIVE-----1184

Qy 589 SONSDQIKLLVTBETGVGIPVDAQGRIFTBPMQADSTSTYGTGTGIGLSISKELVELM 648

Db 1185 -QQNDVVLRFSVRDSGIGLTQEQQSKLFKFTQADTSTTRKYGGTGLGLAISQOLVELM 1243

Qy 649 QGEMGFVSEPGIGSTFSTGVFGKAEINTSITKLERFDLAIQEPFTGLRALVIDNENIRAE 708

Db 1244 GGSIGVESQLGHGSTFFPT-----VKLCISSGQKLVG-QELDGMKILVADDNATARD 1295

Qy 709 VTRYELRLGISADIVSSLRMACTCISKLENLAMILIDKAMNKEPFSVLDELFTRSKV 768

Db 1296 IMRTTLESMPNVDVTRSGDEAIMRC--SQOEYAVALIDWPNLDGIETAKIKQOTK- 1352

Qy 769 TFTRVPKIFLLATSATLTERSEMSTGLIDEVWIKPLRMSVLI CCLQETLVNGKKRQENR 828

Db 1353 ---NAPRILMVSANQDFLQIEQLGLAG-YISKPTISASRLDGINMALGRSGILPVRR 1408

Qy 829 QRRNLGH----LLREKQILVVDDNLVNRRAEGALKKYGAIVTCVESGKAALMKPPHN 884

Db 1409 HQDNIAPELLPLKGRILLVEDNEMNLEVATEFLEQVGIILSIATNGQIALDKL-AQOS 1467

Qy 885 PDACFMDLQMPMDGFETRVRERELERINKKIASGEVSAEMFCXFSSSHVPIIAMTADV 944

Db 1468 PDLVLMDCQMPMDGYQATKAIRO-----RPELA-----QLPVIAMTANA 1507

Qy 945 IQATHEECMKCGMDGYVSKPDEEVEVLYTAVARF 977

Db 1508 MAGDKEMCLRAGMNDHIAKPIEVNLLYQTLUKY 1540

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PR 21-APR-1999; 99US-0130449.
PR 23-APR-1999; 99US-0130510.
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PR 28-APR-1999; 99US-0131449.
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Best Local Similarity 100.0%; Pred. No. 0;			
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Db	152	KARGERKRVHLEALAPKKOQRAQTSRGAGRWKKNILLGILGGVSFSVWVWMDTNE	211
QY	61	BIIMKRRETLANCDERARVLQDQFNVLNHNHVALSILVSTPHHGKIPSAIDQRTFEBYT	120
Db	212	BIIMKRRETLANCDERARVLQDQFNVLNHNHVALSILVSTPHHGKIPSAIDQRTFEBYT	271
QY	121	ERTNERPLTSGVAVALKVPHERKEKEHGWAIKKMETEDQTVVQCVCPENFPDPAIQ	180
Db	272	ERTNERPLTSGVAVALKVPHERKEKEHGWAIKKMETEDQTVVQCVCPENFPDPAIQ	331
QY	181	DEYAVVIFAQETVSHIVSDMMSGEDRENILRASAQKGVLTSPFKLLKSNHLGVLTTF	240
Db	332	DEYAVVIFAQETVSHIVSDMMSGEDRENILRASAQKGVLTSPFKLLKSNHLGVLTTF	391
QY	241	AVYDTSLLPDATERORVEATIGVLGASVDMPSLVEKLHLQASKOTIAVDVYDTNTSGL	300
Db	392	AVYDTSLLPDATERORVEATIGVLGASVDMPSLVEKLHLQASKOTIAVDVYDTNTSGL	451
QY	301	IKWYGEIGDISEQHISSLDGDPGRNHEMHCRFKHKLPIPWTAITPISILVLVITFLVGY	360
Db	452	IKWYGEIGDISEQHISSLDGDPGRNHEMHCRFKHKLPIPWTAITPISILVLVITFLVGY	511
QY	361	ILYEAINRIATVEECQKRELKARAAADIAKSQFLATVSHIETPMNGVLGMLKMLMD	420
Db	512	ILYEAINRIATVEECQKRELKARAAADIAKSQFLATVSHIETPMNGVLGMLKMLMD	571
QY	421	TDLDKQMDYATAGSGKDLTSLINEVLDOAKIESGRLEENVPDMRFILDNVSSLLS	480
Db	572	TDLDKQMDYATAGSGKDLTSLINEVLDOAKIESGRLEENVPDMRFILDNVSSLLS	631
QY	481	GKANKEGIELAVYVSSQVDDVVGVDPFRPQIITNLVGNISIKFTQERGHIFISVHLADEV	540
Db	632	GKANKEGIELAVYVSSQVDDVVGVDPFRPQIITNLVGNISIKFTQERGHIFISVHLADEV	691
QY	541	KEPLTIEDAVLKQRIALGCSGETVSGFPNAVNGSWKNFKTCYSTESQNSDQIKLLVT	600
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QY	601	VEDTGVGIPVDAQGRIFTFPFMQADSTSRITYGTTGIGLSISKRLVELMQGEMGFVSEPGI	660
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QY	661	GSTFSFTGVFCKAETNTSITKLERFDLAIQBFOTGLRALVIDNRNIRAEVTRYELRLGIS	720
Db	812	GSTFSFTGVFCKAETNTSITKLERFDLAIQBFOTGLRALVIDNRNIRAEVTRYELRLGIS	871
QY	721	ADIVSSLRMACTCCISKLENAMILIDKDAWNKEEFSVLDELFTRSKVTFTFVPKIFILIA	780
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QY	781	TSATLTERSEMKTGLIDEVVIKPLRMSVLICCLQETLVNGKKQPNRQRNLGHLREK	840
Db	932	TSATLTERSEMKTGLIDEVVIKPLRMSVLICCLQETLVNGKKQPNRQRNLGHLREK	991
QY	841	QILVVDDNLVNRRAEAGALKKYGAIIVTCVBSGKAALAMLKPPHNFDA CFMDLQMPMDGF	900
Db	992	QILVVDDNLVNRRAEAGALKKYGAIIVTCVBSGKAALAMLKPPHNFDA CFMDLQMPMDGF	1051
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Db	1112	VSKPFESEVLYTAVARFFEPCC	1132
RESULT 2			
AAG47089			
ID	AAG47089 standard; Protein; 1176 AA.		
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AC	AAG47089;		
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DT	18-OCT-2000 (first entry)		
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DE	Arabidopsis thaliana protein fragment SEQ ID NO: 59313.		
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KW	Protein identification; signal transduction pathway; metabolic pathway;		
KW	hybridisation assay; genetic mapping; gene expression control; promoter;		
XX	termination sequence.		
OS	Arabidopsis thaliana.		
XX			
PN	EP1033405-A2.		
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PD	06-SEP-2000.		
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PF	25-FEB-2000; 2000EP-0301439.		
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PR	25-FEB-1999; 99US-0121825.		
PR	05-MAR-1999; 99US-0123180.		
PR	09-MAR-1999; 99US-0123548.		
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PR	07-MAY-1999; 99US-0132863.		
PR	11-MAY-1999; 99US-0134256.		
PR	14-MAY-1999; 99US-0134218.		
PR	14-MAY-1999; 99US-0134219.		
PR	14-MAY-1999; 99US-0134221.		

PR 14-MAY-1999;	99US-0134370.	PR 27-JUL-1999;	99US-0145918.
PR 18-MAY-1999;	99US-0134768.	PR 27-JUL-1999;	99US-0145919.
PR 19-MAY-1999;	99US-0134941.	PR 28-JUL-1999;	99US-0145951.
PR 20-MAY-1999;	99US-0135124.	PR 02-AUG-1999;	99US-0146386.
PR 21-MAY-1999;	99US-0135353.	PR 02-AUG-1999;	99US-0146388.
PR 24-MAY-1999;	99US-0135629.	PR 02-AUG-1999;	99US-0146389.
PR 25-MAY-1999;	99US-0136021.	PR 03-AUG-1999;	99US-0147038.
PR 27-MAY-1999;	99US-0136392.	PR 04-AUG-1999;	99US-0147204.
PR 28-MAY-1999;	99US-0136782.	PR 04-AUG-1999;	99US-0147302.
PR 01-JUN-1999;	99US-0137222.	PR 05-AUG-1999;	99US-0147192.
PR 03-JUN-1999;	99US-0137528.	PR 05-AUG-1999;	99US-0147260.
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PR 08-JUN-1999;	99US-0138094.	PR 09-AUG-1999;	99US-0147493.
PR 10-JUN-1999;	99US-0138540.	PR 09-AUG-1999;	99US-0147935.
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PR 16-JUN-1999;	99US-0139452.	PR 12-AUG-1999;	99US-0148341.
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PR 27-JUL-1999;	99US-0145913.	PR 25-OCT-1999;	99US-0161405.

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PR 26-OCT-1999; 99US-0161359.
PR 26-OCT-1999; 99US-0161360.
PR 26-OCT-1999; 99US-0161361.
PR 28-OCT-1999; 99US-0161920.
PR 28-OCT-1999; 99US-0161921.
PR 28-OCT-1999; 99US-0161992.
PR 28-OCT-1999; 99US-0161993.
PR 29-OCT-1999; 99US-0162142.

Query Match 100.0%; Score 5019; DB 21; Length 1176;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 981; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KARGERKEVHLQALAPKQOQRAQTSRSGAGRWKNIILLGILGGVSFVWFWDNE 60
DB 196 KARGERKEVHLQALAPKQOQRAQTSRSGAGRWKNIILLGILGGVSFVWFWDNE 255
QY 61 EIMKRETLANMCDERARVLQDFNVSLNHVHALSILVSTFHGKIPSAIDQRTFEYT 120
DB 256 EIMKRETLANMCDERARVLQDFNVSLNHVHALSILVSTFHGKIPSAIDQRTFEYT 315
QY 121 ERTNFERPLTSGVAYALKVPHSERKEPEKEHGWAIKKMETBDQTVVQDCVPENFDPAIQ 180
DB 316 ERTNFERPLTSGVAYALKVPHSERKEPEKEHGWAIKKMETEDQTVVQDCVPENFDPAIQ 375
QY 181 DEYAPVIPAQTVSHIVSDMMSGEEDRENILRARSKGVLTPFPFKLLKSNHLGVVLT 240
DB 376 DEYAPVIPAQTVSHIVSDMMSGEEDRENILRARSKGVLTPFPFKLLKSNHLGVVLT 435
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DB 436 AVYDTSLPDPDATEQORVEATIGYLQASYDMPSLVEKLLHQLASKQTTAVDVYDVTNTSGL 495
QY 301 IKMYGSBGIDISEQHSISLDFGDSRNHEHCRFKHKLPIPWTAITPISILVLTFLVGY 360
DB 496 IKMYGSBGIDISEQHSISLDFGDSRNHEHCRFKHKLPIPWTAITPISILVLTFLVGY 555
QY 361 ILVEAINRIATVEEDCCQRELKARAAADTAKSQFLATVSHETRTPMGVGLKMLMD 420
DB 556 ILVEAINRIATVEEDCCQRELKARAAADTAKSQFLATVSHETRTPMGVGLKMLMD 615
QY 421 TDLDAKQMDYAQTAHSGSKDLSLNEVLDAKTESGRLELENVDFDMRFLDNNVSSLS 480
DB 616 TDLDAKQMDYAQTAHSGSKDLSLNEVLDAKTESGRLELENVDFDMRFLDNNVSSLS 675
QY 481 GKANEKGIELAVYVSSQVDPVVGDPGRFRQIITNLVNSIKFTQERGHIPISVHLADEV 540
DB 676 GKANEKGIELAVYVSSQVDPVVGDPGRFRQIITNLVNSIKFTQERGHIPISVHLADEV 735
QY 541 KEPLTIEDAVLKQRLALGCSSEGETVSGFPVAVNAGWGNKPKTCYSTESQNSDQIKLLVT 600
DB 736 KEPLTIEDAVLKQRLALGCSSEGETVSGFPVAVNAGWGNKPKTCYSTESQNSDQIKLLVT 795
QY 601 VEDTGVGIPVDAQGRIFTFEPMQADSSTRTYGGTGIGLSISKRLVELMQGEMGVSEPGI 660
DB 796 VEDTGVGIPVDAQGRIFTFEPMQADSSTRTYGGTGIGLSISKRLVELMQGEMGVSEPGI 855
QY 661 GSTSFSTGVFGKARTNITSITKLERFDLAIQFTGLRALVIDNRRNIRAEVTRYLRLGIS 720
DB 856 GSTSFSTGVFGKARTNITSITKLERFDLAIQFTGLRALVIDNRRNIRAEVTRYLRLGIS 915
QY 721 ADIVSSLRMACTCISKLENLAMILIDKQANKEEFSVLDELFTRSKVTFRVPKIFLLA 780
DB 916 ADIVSSLRMACTCISKLENLAMILIDKQANKEEFSVLDELFTRSKVTFRVPKIFLLA 975
QY 781 TSALTTERSEMKSTGLIDEVVIKPLRMSVLICCIQETLVNGKKQPRQRNHLHREK 840
DB 976 TSALTTERSEMKSTGLIDEVVIKPLRMSVLICCIQETLVNGKKQPRQRNHLHREK 1035
QY 841 QILVVDNLNRRVAEGALKKYGAIVTCVSESKAALAMLPKPHNFDACFMDLQMPMDGF 900
DB 1036 QILVVDNLNRRVAEGALKKYGAIVTCVSESKAALAMLPKPHNFDACFMDLQMPMDGF 1095
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QY 901 EATRRVRELEIREINKKIASCVEVSAEMFCCKSSWHPILAMTADVIQATHECMKCGMDGY 960
DB 1096 EATRRVRELEIREINKKIASCVEVSAEMFCCKSSWHPILAMTADVIQATHECMKCGMDGY 1155
QY 961 VSKPFEEVLYTAVARFEFC 981
DB 1156 VSKPFEEVLYTAVARFEFC 1176

RESULT 3
ABG70781
ID ABG70781 standard; Protein; 1176 AA.
XX
AC ABG70781;
XX
DT 09-DEC-2002 (first entry)
XX
DE A. thaliana cytokinin receptor, AHK2, protein.
XX
KW AHK2; plant; antagonist; agonist; cytokinin receptor;
KW receptor; signal transduction; histidine kinase; hormone; cell division;
KW cell differentiation; agriculture; growth regulator; harvest.
XX
OS Arabidopsis thaliana.
XX
FH Key Location/Qualifiers
FT Region 50..1176
FT /note= "This region is specifically claimed in Claim 1"
FT Region 196..1176
FT /note= "This region is specifically claimed in Claim 1"
XX
FN EPI241182-A2.
XX
PD 18-SEP-2002.
XX
PF 13-MAR-2002; 2002EP-0005749.
XX
PR 15-MAR-2001; 2001JP-0073812.
PR 29-JUN-2001; 2001JP-0198639.
PR 29-JUN-2001; 2001JP-0198640.
XX
PA (SUMO ) SUMITOMO CHEM CO LTD.
XX
PI Kakimoto T, Higuchi M, Inoue T;
XX
DR WPI; 2002-693041/75.
DR N-PSDB; ABS54450.
XX
PT Analyzing agonist or antagonist activity of a substance for use as a
PT plant growth regulator, comprises measuring intracellular signal
PT transduction from a cytokinin receptor expressed in a cell contacted
PT with the test substance -
XX
PS Claim 1; Page 26-28; 47pp; English.
XX
CC The invention discloses a method for analysing antagonist or agonist
CC activity to a cytokinin receptor. The method comprises bringing a
CC candidate substance into contact with a transformed cell, in which a DNA
CC encoding the receptor has been introduced, and then measuring the
CC existence, or the quantity, of the intracellular signal transduction from
CC the receptor expressed in the cell. The cytokinin receptor comprises an
CC extracellular region of the receptor, transmembrane regions, a histidine
CC kinase region and a receiver region of the kinase. The transmembrane
CC regions and kinase region are homogeneous to each other and the receptor
CC region is heterogeneous to them. Cytokinins are plant hormones relevant
CC to cell division and differentiation of higher plants. The method is used
CC for analysing agonist or antagonist activity to a cytokine receptor. A
CC substance with agonist or antagonist activity to the receptor can be
CC used, in agriculture, as a plant growth regulator, e.g. after harvest.
CC The advantage is that the candidate substances do not need to be prepared
CC in such large amounts as in previous methods and that the method avoids
CC the immensely long time to observe and evaluate the growth of the plant
CC and the physiological changes of the plant after spraying. The sequence
```

CC presented is the A. thaliana cytokinin receptor, AHK2, protein.

1	K	A	R	G	E	K	E	K	H	L	O	E	A	L	P	K	Q	O	O	A	O	T	S	R	C	A	G	R	K	N	I	L	L	G	I	L	G	V	S	F	S	V	W	F	W	T	N	E	60									
196	K	A	R	G	E	K	E	K	H	L	O	E	A	L	P	K	Q	O	O	A	O	T	S	R	C	A	G	R	K	N	I	L	L	G	I	L	G	V	S	F	S	V	W	F	W	T	N	E	255									
61	E	I	I	M	K	R	E	T	L	A	N	M	C	D	E	R	A	R	V	L	O	D	Q	F	N	V	S	L	N	H	V	H	A	L	S	I	I	V	S	T	F	H	G	K	I	P	S	A	I	D	Q	R	T	F	E	Y	T	120
256	E	I	I	M	K	R	E	T	L	A	N	M	C	D	E	R	A	R	V	L	O	D	Q	F	N	V	S	L	N	H	V	H	A	L	S	I	I	V	S	T	F	H	G	K	I	P	S	A	I	D	Q	R	T	F	E	Y	T	315
121	E	R	T	N	F	E	R	P	L	T	S	G	V	A	I	A	L	K	V	P	H	S	E	R	E	K	E	K	H	G	N	A	I	K	M	E	T	B	Q	T	V	Q	C	P	N	F	D	P	A	I	Q	180						
316	E	R	T	N	F	E	R	P	L	T	S	G	V	A	I	A	L	K	V	P	H	S	E	R	E	K	E	K	H	G	N	A	I	K	M	E	T	B	Q	T	V	Q	C	P	N	F	D	P	A	I	Q	375						
181	D	E	V	A	P	V	I	F	A	O	B	T	V	S	H	I	V	S	D	M	S	E	E	D	E	R	N	I	L	R	A	S	K	G	V	L	T	S	P	E	K	L	K	N	H	L	G	V	L	T	P	240						
376	D	E	V	A	P	V	I	F	A	O	B	T	V	S	H	I	V	S	D	M	S	E	E	D	E	R	N	I	L	R	A	S	K	G	V	L	T	S	P	E	K	L	K	N	H	L	G	V	L	T	P	435						
241	A	V	Y	D	T	S	L	P	P	D	A	T	E	B	Q	R	V	E	A	T	I	G	L	A	S	Y	D	M	P	S	L	V	E	K	L	L	H	L	Q	A	S																	

Db	1156	VSKPFEVLYTAVARFEPCC	1176
RESULT 4			
AAE33692			
ID	AAE33692	standard; Protein; 1176 AA.	
XX	AC	AAE33692;	
XX	DT	16-APR-2003 (first entry)	
XX	XX	Arabidopsis thaliana histidine kinase 2 (AHK2) protein.	
XX	DE		
XX	KW	Shoot formation; senescence; transgenic; transgenic plant; agriculture;	
XX	KW	cell proliferation; shoot meristem formation; leaf development; AHK;	
XX	KW	photosynthesis; histidine kinase; enzyme.	
XX	OS	Arabidopsis thaliana.	
XX	XX		
XX	FN	WO200299079-A2.	
XX	XX		
XX	PD	12-DEC-2002.	
XX	XX		
XX	PF	06-JUN-2002; 2002WO-US18066.	
XX	XX		
XX	PR	06-JUN-2001; 2001US-296554P.	
XX	XX		
XX	FA	(GEHO) GEN HOSPITAL CORP.	
XX	XX		
XX	PI	Sheen J, Hwang I;	
XX	XX		
XX	DR	WPI; 2003-140613/13.	
XX	DR	N-PSDB; AAD51604.	
XX	XX		
PT	PT	Increasing yield in plant, increasing shoot formation in a plant, or	
PT	PT	delaying senescence in a plant such as wheat, rice, maize, barley,	
PT	PT	potato, by using transgenes that regulate cytokinin response -	
XX	XX		
FS	Disclosure;	Page 75-78; 87pp; English.	
XX	XX		
CC	CC	The present invention relates to a novel method of increasing yield in a	
CC	CC	plant, increasing shoot formation or delaying senescence in a plant. The	
CC	CC	method involves introducing into plant cells, a transgene having a B-type	
CC	CC	response regulator operably linked to a promoter functional in plant	
CC	CC	cells to yield transformed plant cells or whose expression reduces the	
CC	CC	expression of A-type response regulator in the cells of the plant and	
CC	CC	regenerating a plant from the transformed cells. The method is useful	
CC	CC	for increasing the yield in a plant, increasing the shoot formation or	
CC	CC	delaying senescence in a plant such as wheat, rice, maize, barley,	
CC	CC	potato, tomato, soybean, tomato, oat, cotton and sunflower. The method	
CC	CC	is useful for variety of agricultural and commercial purposes including	
CC	CC	improving and enhancing photosynthesis, promoting cell proliferation,	
CC	CC	shoot meristem formation, promoting leaf development, increasing crop	
CC	CC	yield, improving crop and ornamental quality and reducing agricultural	
CC	CC	production costs. The present sequence is Arabidopsis thaliana histidine	
CC	CC	kinase 2 (AHK2) protein. This sequence is used to illustrate the method	
CC	CC	of the invention.	
XX	XX		
SQ	Sequence	1176 AA;	
Query Match	100.0%;	Score 5019; DB 24; Length 1176;	
Best Local Similarity	100.0%;	Pred. No. 0;	
Matches	981; Conservative	0; Mismatches	0; Indels
			0; Gaps
Qy	1	KARGERKEKVLQBALPKKQQQAQTSRRGAGRWKKNILLGILGGVSFVSWFWDTNE	60
Db	196	KARGERKEKVLQBALPKKQQQAQTSRRGAGRWKKNILLGILGGVSFVSWFWDTNE	255
Qy	61	EIMMKRETLANCMDEARVLQDFNVSLNHVHALSILVSTFHGKIPSAIDQRTFFBYT	120
Db	256	EIMMKRETLANCMDEARVLQDFNVSLNHVHALSILVSTFHGKIPSAIDQRTFFBYT	315

QY 121 ERTNFERPLTSGVAVALKVPHSERKFKKHEGWAIKKMETEDQTVVQDCVPENFDPAIQ 180
Db 316 ERTNFERPLTSGVAVALKVPHSERKFKKHEGWAIKKMETEDQTVVQDCVPENFDPAIQ 375
QY 181 DEYAPVIFAQTVSHIVSDVMMSGEEDRENILRARASCKGVLTPFPKLLKSNHLGVLTFF 240
Db 376 DEYAPVIFAQTVSHIVSDVMMSGEEDRENILRARASCKGVLTPFPKLLKSNHLGVLTFF 435
QY 241 AVYDTSLLPDATEQORVETATGYLGASVDMPSLVEKLLHQLASKQTIAVDVYDNTTNSGL 300
Db 436 AVYDTSLLPDATEQORVETATGYLGASVDMPSLVEKLLHQLASKQTIAVDVYDNTTNSGL 495
QY 301 IKWYGEISGDISEOHISLIDFGDPSRNHEMCRFKHKLPIPTWATISILVLVITELVGY 360
Db 496 IKWYGEISGDISEOHISLIDFGDPSRNHEMCRFKHKLPIPTWATISILVLVITELVGY 555
QY 361 ILYEAINRIATVEEDCQRMRELKARAAADIAKQFLATVSGHEIRTPMNGVLGMLKMLMD 420
Db 556 ILYEAINRIATVEEDCQRMRELKARAAADIAKQFLATVSGHEIRTPMNGVLGMLKMLMD 615
QY 421 TDLDAKQMDYACTAHGSKDLTSLINEVLDQAKIESGRLELENVPPDMRFILDNVSSLLS 480
Db 616 TDLDAKQMDYACTAHGSKDLTSLINEVLDQAKIESGRLELENVPPDMRFILDNVSSLLS 675
QY 481 GKANEKGIELAVYSSQVDPVVGDPSPFRROIITNLVGNISIKFTQERGHIFISVHLADEV 540
Db 676 GKANEKGIELAVYSSQVDPVVGDPSPFRROIITNLVGNISIKFTQERGHIFISVHLADEV 735
QY 541 KEPLTIEDAVLKQRLALGCSSEGETVSGFPVAVNAGSMKNFKTCYSTESQNSDQIKLLVT 600
Db 736 KEPLTIEDAVLKQRLALGCSSEGETVSGFPVAVNAGSMKNFKTCYSTESQNSDQIKLLVT 795
QY 601 VEDTGVPVDAQGRIFTFPQWQASSTSRITYGGTIGLISISKRLVELMQGEMGFVSEPGI 660
Db 796 VEDTGVPVDAQGRIFTFPQWQASSTSRITYGGTIGLISISKRLVELMQGEMGFVSEPGI 855
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Db 856 GSTSFCTGVCFKATNTSITKLERFDLAIQFTGLRALVIDNRIRAEVTRYELRLGIS 915
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Db 916 ADIVSSLRMACTCCISKLENLAMILIDKDNKKEEFSVLDELFTRSKVTFTVRPKIFLLA 975
QY 781 TSATLTERSEMKSTGLIDEVVIKPLRMSVLICCLQETLVNGKQPNRQRNQLHLLREK 840
Db 976 TSATLTERSEMKSTGLIDEVVIKPLRMSVLICCLQETLVNGKQPNRQRNQLHLLREK 1035
QY 841 QILVVDDNLVNRRAEGALKKYGAIVTCVESGKAALMKPPHNFDA CFMDLQMPMDGF 900
Db 1036 QILVVDDNLVNRRAEGALKKYGAIVTCVESGKAALMKPPHNFDA CFMDLQMPMDGF 1095
QY 901 EATRVRELEREINKKIASGEVSAMEFCFSSWHVPILAMTADVIQATHEECMCGMDGY 960
Db 1096 EATRVRELEREINKKIASGEVSAMEFCFSSWHVPILAMTADVIQATHEECMCGMDGY 1155
QY 961 VSKPFEFEVLVAVARFEPCC 981
Db 1156 VSKPFEFEVLVAVARFEPCC 1176

RESULT 5
AAG47088

ID AAG47088 standard; Protein; 1238 AA.

XX AC AAG47088;

DT 18-OCT-2000 (first entry)

XX Arabidopsis thaliana protein fragment SEQ ID NO: 59312.

DE Protein identification; signal transduction pathway; metabolic pathway;
KW hybridisation assay; Genetic mapping; Gene expression control; promoter;

KW termination sequence.

XX OS Arabidopsis thaliana.

XX PN EP1033405-A2.

XX PD 06-SEP-2000.

XX PF 25-FEB-2000; 2000EP-0301439.

XX PR 25-FEB-1999; 99US-0121825.

PR 05-MAR-1999; 99US-0123180.

PR 09-MAR-1999; 99US-0123548.

PR 23-MAR-1999; 99US-0125788.

PR 25-MAR-1999; 99US-0126264.

PR 29-MAR-1999; 99US-0126785.

PR 01-APR-1999; 99US-0127462.

PR 06-APR-1999; 99US-0128234.

PR 08-APR-1999; 99US-0128714.

PR 16-APR-1999; 99US-0129845.

PR 19-APR-1999; 99US-0130077.

PR 21-APR-1999; 99US-0130449.

PR 23-APR-1999; 99US-0130510.

PR 23-APR-1999; 99US-0130891.

PR 28-APR-1999; 99US-0131449.

PR 30-APR-1999; 99US-0132048.

PR 30-APR-1999; 99US-0132407.

PR 04-MAY-1999; 99US-0132484.

PR 05-MAY-1999; 99US-0132485.

PR 06-MAY-1999; 99US-0132486.

PR 06-MAY-1999; 99US-0132487.

PR 07-MAY-1999; 99US-0132863.

PR 11-MAY-1999; 99US-0134256.

PR 14-MAY-1999; 99US-0134218.

PR 14-MAY-1999; 99US-0134219.

PR 14-MAY-1999; 99US-0134221.

PR 14-MAY-1999; 99US-0134370.

PR 18-MAY-1999; 99US-0134768.

PR 19-MAY-1999; 99US-0134941.

PR 20-MAY-1999; 99US-0135124.

PR 21-MAY-1999; 99US-0135353.

PR 24-MAY-1999; 99US-0135629.

PR 25-MAY-1999; 99US-0136021.

PR 27-MAY-1999; 99US-0136392.

PR 28-MAY-1999; 99US-0136782.

PR 01-JUN-1999; 99US-0137222.

PR 03-JUN-1999; 99US-0137528.

PR 04-JUN-1999; 99US-0137502.

PR 07-JUN-1999; 99US-0137724.

PR 08-JUN-1999; 99US-0138094.

PR 10-JUN-1999; 99US-0138540.

PR 10-JUN-1999; 99US-0138847.

PR 14-JUN-1999; 99US-0139119.

PR 16-JUN-1999; 99US-0139452.

PR 16-JUN-1999; 99US-0139453.

PR 17-JUN-1999; 99US-0139452.

PR 18-JUN-1999; 99US-0139454.

PR 18-JUN-1999; 99US-0139455.

PR 18-JUN-1999; 99US-0139456.

PR 18-JUN-1999; 99US-0139457.

PR 18-JUN-1999; 99US-0139458.

PR 18-JUN-1999; 99US-0139459.

PR 18-JUN-1999; 99US-0139460.

PR 18-JUN-1999; 99US-0139461.

PR 18-JUN-1999; 99US-0139462.

PR 18-JUN-1999; 99US-0139463.

PR 18-JUN-1999; 99US-0139750.

PR 18-JUN-1999; 99US-0139763.

PR 21-JUN-1999; 99US-0139817.

PR 22-JUN-1999; 99US-0139899.

PR 23-JUN-1999; 99US-0140353.

PR 23-JUN-1999; 99US-0140354.

PR 24-JUN-1999; 99US-0140695.

PR	28-JUN-1999;	99US-0140823.	PR	10-SEP-1999;	99US-0153070.
PR	29-JUN-1999;	99US-0140931.	PR	13-SEP-1999;	99US-0153758.
PR	30-JUN-1999;	99US-0141287.	PR	15-SEP-1999;	99US-0154018.
PR	01-JUL-1999;	99US-0141842.	PR	16-SEP-1999;	99US-0154039.
PR	01-JUL-1999;	99US-0142154.	PR	20-SEP-1999;	99US-0154779.
PR	02-JUL-1999;	99US-0142055.	PR	23-SEP-1999;	99US-0155139.
PR	06-JUL-1999;	99US-0142390.	PR	23-SEP-1999;	99US-0155486.
PR	08-JUL-1999;	99US-0142803.	PR	24-SEP-1999;	99US-0155659.
PR	09-JUL-1999;	99US-0142920.	PR	28-SEP-1999;	99US-0156458.
PR	12-JUL-1999;	99US-0142977.	PR	29-SEP-1999;	99US-0156596.
PR	13-JUL-1999;	99US-0143542.	PR	04-OCT-1999;	99US-0157117.
PR	14-JUL-1999;	99US-0143624.	PR	05-OCT-1999;	99US-0157753.
PR	15-JUL-1999;	99US-0144005.	PR	06-OCT-1999;	99US-0157865.
PR	16-JUL-1999;	99US-0144085.	PR	07-OCT-1999;	99US-0158029.
PR	18-JUL-1999;	99US-0144086.	PR	08-OCT-1999;	99US-0158232.
PR	19-JUL-1999;	99US-0144325.	PR	12-OCT-1999;	99US-0158369.
PR	19-JUL-1999;	99US-0144331.	PR	13-OCT-1999;	99US-0158293.
PR	19-JUL-1999;	99US-0144332.	PR	13-OCT-1999;	99US-0159294.
PR	19-JUL-1999;	99US-0144333.	PR	13-OCT-1999;	99US-0159295.
PR	19-JUL-1999;	99US-0144334.	PR	14-OCT-1999;	99US-0159329.
PR	19-JUL-1999;	99US-0144335.	PR	14-OCT-1999;	99US-0159330.
PR	20-JUL-1999;	99US-0144352.	PR	14-OCT-1999;	99US-0159331.
PR	20-JUL-1999;	99US-0144632.	PR	14-OCT-1999;	99US-0159637.
PR	20-JUL-1999;	99US-0144884.	PR	14-OCT-1999;	99US-0159638.
PR	21-JUL-1999;	99US-0144814.	PR	18-OCT-1999;	99US-0159584.
PR	21-JUL-1999;	99US-0145086.	PR	21-OCT-1999;	99US-0160741.
PR	21-JUL-1999;	99US-0145088.	PR	21-OCT-1999;	99US-0160767.
PR	22-JUL-1999;	99US-0145085.	PR	21-OCT-1999;	99US-0160768.
PR	22-JUL-1999;	99US-0145087.	PR	21-OCT-1999;	99US-0160770.
PR	22-JUL-1999;	99US-0145089.	PR	21-OCT-1999;	99US-0160814.
PR	22-JUL-1999;	99US-0145192.	PR	21-OCT-1999;	99US-0160815.
PR	23-JUL-1999;	99US-0145145.	PR	22-OCT-1999;	99US-0160980.
PR	23-JUL-1999;	99US-0145218.	PR	22-OCT-1999;	99US-0160981.
PR	23-JUL-1999;	99US-0145224.	PR	22-OCT-1999;	99US-0160989.
PR	26-JUL-1999;	99US-0145276.	PR	25-OCT-1999;	99US-0161404.
PR	27-JUL-1999;	99US-0145913.	PR	25-OCT-1999;	99US-0161405.
PR	27-JUL-1999;	99US-0145918.	PR	25-OCT-1999;	99US-0161406.
PR	27-JUL-1999;	99US-0145919.	PR	26-OCT-1999;	99US-0161359.
PR	28-JUL-1999;	99US-0145951.	PR	26-OCT-1999;	99US-0161360.
PR	02-AUG-1999;	99US-0146386.	PR	26-OCT-1999;	99US-0161361.
PR	02-AUG-1999;	99US-0146388.	PR	28-OCT-1999;	99US-0161920.
PR	03-AUG-1999;	99US-0146389.	PR	28-OCT-1999;	99US-0161992.
PR	04-AUG-1999;	99US-0147038.	PR	28-OCT-1999;	99US-0161993.
PR	04-AUG-1999;	99US-0147204.	PR	29-OCT-1999;	99US-0162142.
PR	04-AUG-1999;	99US-0147302.	Query Match 100.0%; Score 5019; DB 21; Length 1238;		
PR	05-AUG-1999;	99US-0147192.	Best Local Similarity 100.0%; Pred. No. 0;		
PR	05-AUG-1999;	99US-0147260.	Matches 981; Conservative 0; Mismatches 0; Indels 0; Gaps 0;		
PR	06-AUG-1999;	99US-0147303.	QY 1 KARGERKEKVHLQELALPKKQOQRAQTSRGAGRWKKNILLGILGGVSFSVWFWDTNE 60		
PR	06-AUG-1999;	99US-0147416.	258 KARGERKEKVHLQELALPKKQOQRAQTSRGAGRWKKNILLGILGGVSFSVWFWDTNE 317		
PR	09-AUG-1999;	99US-0147493.	QY 61 EIIIMKRRETLANCMDEARVLOQPNVSLNHVHALSILVSTPHHKIPSAIDORTFEYTT 120		
PR	10-AUG-1999;	99US-0147935.	318 EIIIMKRRETLANCMDEARVLOQPNVSLNHVHALSILVSTPHHKIPSAIDORTFEYTT 377		
PR	11-AUG-1999;	99US-0148171.	QY 121 ERTNFERPLTSGVAYALKVPHSERKEFEKHGWAIIKKMETEDQTVVQDCVPENFDPAPIQ 180		
PR	12-AUG-1999;	99US-0148341.	378 ERTNFERPLTSGVAYALKVPHSERKEFEKHGWAIIKKMETEDQTVVQDCVPENFDPAPIQ 437		
PR	13-AUG-1999;	99US-0148565.	QY 181 DEYAPVIFAQETVSHIVSDMMSGEDRENILRARASGKGVLTSPFKLLKSNHLGVLTFF 240		
PR	13-AUG-1999;	99US-0148684.	438 DEYAPVIFAQETVSHIVSDMMSGEDRENILRARASGKGVLTSPFKLLKSNHLGVLTFF 497		
PR	16-AUG-1999;	99US-0149368.	QY 241 AVYDTSLLPPDATEQORVEATIGYLGAQYDMPSLVEKLLHQLASKQTIADVVDYDTNTSGL 300		
PR	17-AUG-1999;	99US-0149175.	498 AVYDTSLLPPDATEQORVEATIGYLGAQYDMPSLVEKLLHQLASKQTIADVVDYDTNTSGL 557		
PR	18-AUG-1999;	99US-0149426.	QY 301 IKWYGEIGDISEQHISSLDGDPNRNHEMCRFKHKLPIPWTAITPSILVILVITFLVGY 360		
PR	20-AUG-1999;	99US-0149722.	558 IKWYGEIGDISEQHISSLDGDPNRNHEMCRFKHKLPIPWTAITPSILVILVITFLVGY 617		
PR	20-AUG-1999;	99US-0149723.			
PR	20-AUG-1999;	99US-0149929.			
PR	23-AUG-1999;	99US-0149902.			
PR	23-AUG-1999;	99US-0149930.			
PR	25-AUG-1999;	99US-0150566.			
PR	26-AUG-1999;	99US-0150884.			
PR	27-AUG-1999;	99US-0151065.			
PR	27-AUG-1999;	99US-0151066.			
PR	27-AUG-1999;	99US-0151080.			
PR	30-AUG-1999;	99US-0151303.			
PR	31-AUG-1999;	99US-0151438.			
PR	01-SEP-1999;	99US-0151930.			
PR	07-SEP-1999;	99US-0152363.			

Db 616 TDLDAKQMDYAQTAHSGKDLTSLINEVLDQAKIESGRLELENVPPDMRFILDNVSSLLS 675
QY 481 GRANEXGIELAVYVSSQVDPVVVGDPSRFRQIITNLVGNISIKFTQERGHIFISVHLADEV 540
Db 676 GRANEXGIELAVYVSSQVDPVVVGDPSRFRQIITNLVGNISIK--ERGHIFISVHLADEV 732
QY 541 KEPLTIEDAVLKQRIALGCGSEGETVSGPPAVNAGSWKNFKTCYSTESQNSDQIKLVT 600
Db 733 KEPLTIEDAVLKQRIALGCGSEGETVSGPPAVNAGSWKNFKTCYSTESQNSDQIKLVT 792
QY 601 VEDTGVGIPVDAQGRIFTFPMQADSTSRTYGTTGIGLSISKRLVELMQGEMGFVSEPCI 660
Db 793 VEDTGVGIPVDAQGRIFTFPMQADSTSRTYGTTGIGLSISKRLVELMQGEMGFVSEPCI 852
QY 661 GSTFSFTGVFGKAETNTSITKLERFDLAIQEBFTGLRALVIDNRNIRAETRYELRRLGIS 720
Db 853 GSTFSFTGVFGKAETNTSITKLERFDLAIQEBFTGLRALVIDNRNIRAETRYELRRLGIS 912
QY 721 ADIVSSLRMACTCCISKLENLAMILIDKDAWNKEEFSVLDELFTRSKVTFTRPVKIFLLA 780
Db 913 ADIVSSLRMACTCCISKLENLAMILIDKDAWNKEEFSVLDELFTRSKVTFTRPVKIFLLA 972
QY 781 TSATLTERSEMKSTGLIDEVWIKPLRMSVLICCLQETLVNGKKROPNRNIGHLLREK 840
Db 973 TSATLTERSEMKSTGLIDEVWIKPLRMSVLICCLQETLVNGKKROPNRNIGHLLREK 1032
QY 841 QILVVDNVLNRRVARGALKKYGAIVTCVESGKAALAMLKPPHNFDA CFMDLQMPMDGF 900
Db 1033 QILVVDNVLNRRVARGALKKYGAIVTCVESGKAALAMLKPPHNFDA CFMDLQMPMDGF 1092
QY 901 EATRVRVLEIREINKKIAGEVSAEMFCFSSWHVPILAMTADVIQATHEBCKMCMQDGY 960
Db 1093 EATRVRVLEIREINKKIAGEVSAEMFCFSSWHVPILAMTADVIQATHEBCKMCMQDGY 1152
QY 961 VSKPREEEVLVTAVARFFBPC 981
Db 1153 VSKPREEEVLVTAVARFFBPC 1173
RESULT 7
ID ABB93625 standard; Protein; 1173 AA.
XX AC ABB93625;
XX DT 31-MAY-2002 (first entry)
XX DE Herbicidally active polypeptide SEQ ID NO 2836.
XX KW Herbicidal; plant; agriculture; herbicide.
XX OS Arabidopsis thaliana.
XX PN WO200210210-A2.
XX PD 07-FEB-2002.
XX PF 28-AUG-2001; 2001WO-EP09892.
XX PR 28-AUG-2001; 2001WO-EP09892.
XX PA (FARB) BAYER AG.
XX PI Tietjen K, Weidler M;
XX DR WPI; 2002-269010/31.
XX PT Identifying plant target proteins for herbicidally active compounds,
XX PT comprising aligning and comparing nucleic acid or amino acid sequences
XX PT from plant with nucleic acid or amino acid sequences from non-plant
XX PT organisms -

PS Claim 5; SEQ ID NO 2836; 261pp + Sequence Listing; English.
XX CC The invention relates to identifying target proteins
CC (ABB9790-ABB94016) for herbicidally active compounds, comprising
CC aligning and comparing nucleic acid or amino acid sequences from plant
CC with nucleic acid or amino acid sequences from non-plant organisms using
CC suitable search parameters, where plant sequences having an E-value
CC greater by a factor of 3 than the E-value of most similar non-plant
CC sequences are selected. The polypeptides or nucleic acids encoding them
CC are useful for identifying modulators. The identified modulators are
CC useful as herbicides.
XX Sequence 1173 AA;
SQ Query Match 99.5%; Score 4991.5; DB 23; Length 1173;
Best Local Similarity 99.7%; Pred. No. 0;
Matches 978; Conservative 0; Mismatches 0; Indels 3; Gaps 1;
QY 1 KARGERKEKVLHLEALAPKQOQRAQTSRGAGRWKKNILLGILGGVSFSVWFMDTNE 60
Db 196 KARGERKEKVLHLEALAPKQOQRAQTSRGAGRWKKNILLGILGGVSFSVWFMDTNE 255
QY 61 EIIKMRRETLANMCDERARVLQDPNVSLNHVHALSILVSTPHGKIPSAIDORTFEYVT 120
Db 256 EIIKMRRETLANMCDERARVLQDPNVSLNHVHALSILVSTPHGKIPSAIDORTFEYVT 315
QY 121 ERTNERPLTSGVAVALKVPHSERKEKPEHGWAIKKMETEDQTVVQDCVPENFPAPIQ 180
Db 316 ERTNERPLTSGVAVALKVPHSERKEKPEHGWAIKKMETEDQTVVQDCVPENFPAPIQ 375
QY 181 DEYAVPIVFAQETVSHIVSDMMSGEDRENILRAFASGKGLTSPFKLLKSNHGLVLTFF 240
Db 376 DEYAVPIVFAQETVSHIVSDMMSGEDRENILRAFASGKGLTSPFKLLKSNHGLVLTFF 435
QY 241 AVYDTSLPDATEORVEATIGYLCA SYDMPSLVEKLHLQASKOTIAVDVDTTNTSGL 300
Db 436 AVYDTSLPDATEORVEATIGYLCA SYDMPSLVEKLHLQASKOTIAVDVDTTNTSGL 495
QY 301 IKMYGSEIGDISQHISSLDFGDPSPRNHEMCRFKHKLPIPMWTAITPSILVILVITFLVGY 360
Db 496 IKMYGSEIGDISQHISSLDFGDPSPRNHEMCRFKHKLPIPMWTAITPSILVILVITFLVGY 555
QY 361 ILYEAINRIATVEEDCQKRELKARAEAAADIAKSOFLATVSHIERTPMNGVLGMLKMLMD 420
Db 556 ILYEAINRIATVEEDCQKRELKARAEAAADIAKSOFLATVSHIERTPMNGVLGMLKMLMD 615
QY 421 TDLDAKQMDYAQTAHSGKDLTSLINEVLDQAKIESGRLELENVPPDMRFILDNVSSLLS 480
Db 616 TDLDAKQMDYAQTAHSGKDLTSLINEVLDQAKIESGRLELENVPPDMRFILDNVSSLLS 675
QY 481 GRANEXGIELAVYVSSQVDPVVVGDPSRFRQIITNLVGNISIKFTQERGHIFISVHLADEV 540
Db 676 GRANEXGIELAVYVSSQVDPVVVGDPSRFRQIITNLVGNISIK--ERGHIFISVHLADEV 732
QY 541 KEPLTIEDAVLKQRIALGCGSEGETVSGPPAVNAGSWKNFKTCYSTESQNSDQIKLVT 600
Db 733 KEPLTIEDAVLKQRIALGCGSEGETVSGPPAVNAGSWKNFKTCYSTESQNSDQIKLVT 792
QY 601 VEDTGVGIPVDAQGRIFTFPMQADSTSRTYGTTGIGLSISKRLVELMQGEMGFVSEPCI 660
Db 793 VEDTGVGIPVDAQGRIFTFPMQADSTSRTYGTTGIGLSISKRLVELMQGEMGFVSEPCI 852
QY 661 GSTFSFTGVFGKAETNTSITKLERFDLAIQEBFTGLRALVIDNRNIRAETRYELRRLGIS 720
Db 853 GSTFSFTGVFGKAETNTSITKLERFDLAIQEBFTGLRALVIDNRNIRAETRYELRRLGIS 912
QY 721 ADIVSSLRMACTCCISKLENLAMILIDKDAWNKEEFSVLDELFTRSKVTFTRPVKIFLLA 780
Db 913 ADIVSSLRMACTCCISKLENLAMILIDKDAWNKEEFSVLDELFTRSKVTFTRPVKIFLLA 972
QY 781 TSATLTERSEMKSTGLIDEVWIKPLRMSVLICCLQETLVNGKKROPNRNIGHLLREK 840
Db 973 TSATLTERSEMKSTGLIDEVWIKPLRMSVLICCLQETLVNGKKROPNRNIGHLLREK 1032

Db	965	KRIKNGEALIVENGKNTSWHLPVILANTADVIQATHEECLKCGMDGVYSKPEAEQLYREV	1024
QY	975	ARFF 978	
Db	1025	SRFF 1028	
RESULT 9			
ID	AAE33693	AAE33693 standard; Protein; 1036 AA.	
XX	AC	AAE33693;	
XX	DT	16-APR-2003 (first entry)	
XX	DE	Arabidopsis thaliana histidine kinase 3 (AHK3) protein.	
KW	KW	Shoot formation; senescence; transgenic; transgenic plant; agriculture; call proliferation; shoot meristem formation; leaf development; AHK;	
KW	KW	photosynthesis; histidine kinase; enzyme.	
XX	OS	Arabidopsis thaliana.	
XX	PN	WO200299079-A2.	
XX	XX		
PD	XX	12-DEC-2002.	
XX	XX		
PF	XX	06-JUN-2002; 2002WO-US18066.	
XX	XX		
PR	XX	06-JUN-2001; 2001US-296554P.	
XX	XX		
PA	XX	(GEO) GEN HOSPITAL CORP.	
XX	XX		
PI	XX	Sheen J, Hwang I;	
XX	XX		
DR	XX	WPI; 2003-140613/13.	
XX	XX		
PT	XX	Increasing yield in plant, increasing shoot formation in a plant, or	
PT	XX	delaying senescence in a plant such as wheat, rice, maize, barley,	
PT	XX	potato, by using transgenes that regulate cytokinin response -	
XX	XX		
PS	XX	Disclosure; Page 78-80; 87pp; English.	
XX	XX		
CC	XX	The present invention relates to a novel method of increasing yield in a	
CC	XX	plant, increasing shoot formation or delaying senescence in a plant. The	
CC	XX	method involves introducing into plant cells, a transgene having a B-type	
CC	XX	response regulator operably linked to a promoter functional in plant	
CC	XX	cells to yield transformed plant cells or whose expression reduces the	
CC	XX	expression of A-type response regulator in the cells of the plant and	
CC	XX	regenerating a plant from the transformed cells. The method is useful	
CC	XX	for increasing the yield in a plant, increasing the shoot formation or	
CC	XX	delaying senescence in a plant such as wheat, rice, maize, barley,	
CC	XX	potato, tomato, soybean, tomato, oat, cotton and sunflower. The method	
CC	XX	is useful for variety of agricultural and commercial purposes including	
CC	XX	improving and enhancing photosynthesis, promoting cell proliferation,	
CC	XX	shoot meristem formation, promoting leaf development, increasing crop	
CC	XX	yields, improving crop and ornamental quality and reducing agricultural	
CC	XX	production costs. The present sequence is Arabidopsis thaliana histidine	
CC	XX	kinase 3 (AHK3) protein. This sequence is used to illustrate the method	
CC	XX	of the invention.	
XX	XX		
SQ	XX	Sequence 1036 AA;	
Query Match 53.5%; Score 2685.5; DB 24; Length 1036;			
Best Local Similarity 57.2%; Pred. No. 1.3e-225;			
Matches 551; Conservative 142; Mismatches 224; Indels 47; Gaps 13;			
QY	35	WRKNILLGLGVSVVWFWDTEETIMKRETIANCMDEARVLOQFNVSLNHVUA	94
Db	92	WRK-LVVVWFVWLVSITWTFVSSQAMEKRETIANCMDEARVLOQFNVSLNHVUA	150
QY	95	LSILVSTFHGKIIPSAIDQRTFEYTERTNFRPLTSGVAYALKVPHSEREFKEHGA	154

Db	151	MSILISTFHGKIIPSAIDORTFEYTERTNFRPLTSGVAYAMRVLHSEBEFEQOQWT	210
QY	155	IKKMETEDQTVV--QDCVPENFDPAIQDEYAPVIFAQETVSHVIVSDMMGSEEDRENIL	212
Db	211	IRKMYSLQNPHKDDYDLEALESPVQEEYAPVIFAQDTVSHVSLDMLSGKEDRENVL	270
QY	213	PARASGKGVLTSPFKLLKSNHGLVLTFAVYDTSIPPDATBEQORVEATIGVLSYDMP	272
Db	271	RARSSGKGVLTAPFPLIKTNRLGVLTFAVYKRDLPFNATPKERTEATNGVILGGVFDES	330
QY	273	LVEKLLHQLASKOTTIAVDYDTNTSGLIKMYGSGIDISEQHSLSLDFGDPSSRHEMHC	332
Db	331	LVENLLQLASKQTLVNVYDITNHSQPSIMYTNVSADGLERVSPILFGDPLRKHWR	390
QY	333	RPKHLPIPTWATPISILVLTFLVYILVEAINRIATVEEDCQKRELKARABADIA	392
Db	391	RFKQPPFVLSMTVSFGILVALIAHIHATVSRIHKVBEDCDKMLKKKAAADVA	450
QY	393	KSQFLATVSHRIETPMGVGLKMLMDTDLDKADMDYAQTAKHSGKDLTSLINEVLOA	452
Db	451	KSQFLATVSHRIETPMGVGLKMLMDTDLDVTDYVTAQAAGKALVSLINEVLOA	510
QY	453	KIESGRLELENVDFMRFILDNVSSLLSGKANEKIEIAVYVSSQVDPVWDGDSRFRQI	512
Db	511	KIESCKLELEVRFDLGLDDVLSFKSKQKGVLAIVISDRVPMGLDGPFRFQI	570
QY	513	ITNLVNSIKFTQBERGHIFISVHLADRYKEPLTIEDAVLKQRLALGCGSESETVSGFPAV	572
Db	571	LTNLMGNSIKFT-EGHIFVTVHLVDLFEISIDGETA-----SSPESTLSGLPVA	619
QY	573	NAWGSKNFKCYSTESQNS-----DQIKLAVTVEDTGVIPVDAQGRIFTFPMQADST	627
Db	620	DRQRWENFK-AFSSNGHRSFEPSPDINLIVSVEDTGVGIPVEAQSRIFTTFMQVGPSI	678
QY	628	SRTYGTGTIGLSISKRLVELMQGEMGFVSEPGIGSTFTSGTGVFG-----KAETNTSI	679
Db	679	SRTYGTGTIGLSISKRLVELMQGEMGFVSEPGIGSTFTSGTGVFG-----KAETNTSI	738
QY	680	TYLERFDLAIQBTGLRALVDNIRAEVTRYELRRLIGISADIVSSLRMACTCISKLE	739
Db	739	-----FSEFRGMKAVVDHRRPARAKVSWYHFQRLGIRVEVVRVEQALHYLKIGTT	789
QY	740	NLAMILDKDANKKEEFSVLDELFTSRKVTRVTKIPLATSATLTERSEMKSTGLIDE	799
Db	790	TVMNLIEQEIWNREADDFIKKL---QKDPLFLSPKILLANSVB--SSISEALCTG-IDP	844
QY	800	--VVIKPLRMSVLIICLOETLVNGKKRPNRQ---RRNLGHLRLREKQILVDDNLRVR	854
Db	845	PIVIVKPLRASWLAATLQRLGIGIREPPQHKGPALLIRNLLGKRLIVDDNNVLRV	904
QY	855	REGALKYGAIVTCVESGAALAMKPPHNFDAFMDLQMPMDGFATRRVRELEIREIN	914
Db	905	AAGALKYGAIVTCVESGAALAMKPPHNFDAFMDLQMPMDGFATRRVRELEIREIN	964
QY	915	KKIASGEVSAEMFCKFFSSWHVPILAMTADVQATHEECMKCMGDCGVSKPPEEVLVYAV	974
Db	965	KKIKNGEALIVENGKNTSWHLPVILANTADVIQATHEECLKCGMDGVVSKPFAEQLYREV	1024
QY	975	ARFF 978	
Db	1025	SRFF 1028	
RESULT 10			
ID	AAO22567	AAO22567 standard; Protein; 1092 AA.	
XX	AC	AAO22567;	
XX	DT	28-OCT-2002 (first entry)	
XX	DE	Wooden leg (WOL) gene related protein SEQ ID No 18.	

CC activity to a cytokinin receptor. The method comprises bringing a
CC candidate substance into contact with a transformed cell, in which a
CC encoding the receptor has been introduced, and then measuring the
CC existence, or the quantity, of the intracellular signal transduction from
CC the receptor expressed in the cell. The cytokinin receptor comprises an
CC extracellular region of the receptor, a transmembrane regions, a histidine
CC kinase region and a receiver region of the kinase. The transmembrane
CC regions and kinase region are homogeneous to each other and the receptor
CC region is heterogeneous to them. Cytokinins are plant hormones relevant
CC to cell division and differentiation of higher plants. The method is used
CC for analysing agonist or antagonist activity to a cytokine receptor. A
CC substance with agonist or antagonist activity to the receptor can be
CC used, in agriculture, as a plant growth regulator, e.g. after harvest.
CC The advantage is that the candidate substances do not need to be prepared
CC in such large amounts as in previous methods and that the method avoids
CC the immensely long time to observe and evaluate the growth of the plant
CC and the physiological changes of the plant after spraying. The sequence
CC presented is the A. thaliana cytokinin receptor, CRE1, protein.
XX
SQ Sequence 1057 AA;

Query Match 50.7%; Score 2545.5; DB 23; Length 1057;
Best Local Similarity 53.3%; Pred. No. 2.5e-213;
Matches 538; Conservative 152; Mismatches 239; Indels 81; Gaps 17;
4 GERKEKVLQEE--ALAPKKQQAQTSRRGAGRWKXNILLGILGGVSFVW-WFWDTNE 60
89 GNKKGSTFIQEHRAALLPKAL-----LWIIIVGFSSGIYQWMDANK 131
61 EIMKRETLANMCDERARVLQDFNVSLNHALSILVSTFHHGKIPSAIDQTFREYT 120
132 ---IRREBEVLVSMCDQARMLQDFSVNVHVALILVSTFHHKPNPSAIDQETFAEYT 198
121 ERINFERPLSGVAYALKVPHSREKEKEHWAUKWETEDQTVQDCVPENPDPAIQ 180
189 ARTAFERPLSGVAYAEKVVNFREMERQHNWIKTM-----DRGEPSVR 235
181 DEYAPVIFAQETVSHIVSDVMGSEEDRENILARASGKGLTSPFKLLKSNHGLVLT 240
236 DEYAPVIFSQDSVYLSLDMGSEEDRENILARARETGKAVLTSPFKLLETHLGVLT 295
241 AVYDTSLPDDEQREVEATIGYLGASDYDPSLVEKLLHQLASKQTIADVDTTNTSGL 300
296 PVYKSSLPENPTVEERIAATAGYLGAFDVSIVENLLGLAGNALVHVYDITNASDP 355
301 IKWYGS--ETGDTISEQHSISLDPGSPRNHMHCRFKHKLPIPWTAITPSILVLITFLV 358
356 LVNMGNDDEADRSLSHESKLDFGDPFRKHMTICRVHOKAPIPLNVLTTVPFLFAIGFLV 415
359 GYILYEAINRIATVEEDCKRMRELKARAEADIAKSOFLATVSHEIRTPMNGVLMKML 418
416 GYILYGAAHVIKVEDDFHEMQELKTRAADVAKSOFLATVSHEIRTPMNGILGMLAM 475
419 MDTDLDAQMDYAQTAHSGKOLITSLINEVDQAKTESGRLELENVPPDMFRILDNVSSL 478
476 LDTELSSTORDYAQTAQVCGKALIALINEVLDRAKIEAGKLELESVPPFDIRSLDDVLSL 535
479 LSKANEGHELAVYSSQVDPVVDGSPFRQITNLVNSNKTQERGHIFISVHLAD 538
536 FSEESNKGIELAVFVSDKVPFVKGDSGRFRQITNLVNSNKTQERGHIFVSVHLAE 594
539 EVK--EPL-TIEDAVLKQRLALGCSSEGTGVSFPFVAVNANGSKWKNFKTCYSTESQNSD- 593
595 QSKDESEPKNALGGVSEEMIVVSKQSYNTLSGYEAADGRNSWDGFKHLVSEQSLSEF 654
594 ----QIKLLVVBEDTGVGIPVDAQGRIFTPFMQADSTSTRTYGGTIGLISISKRLVELMQ 649
655 DISSNVLNMSIEDTGIGIPVAGQGVFEMFQADSTSTSTNYGGTIGLISISKRLVELMR 714
650 GEMGFVSEPGIGTFTGFTGFGKAENNTSTIKLER--FDLAIQETGLRALVIDNRNIRA 707
715 GQINFISRPHIGTFTFTAVLEKCDKCSAINEMKKNVHELPSTFGKMAIVDAKPVRA 774

QY 708 EVTRYELRLGISADIVSSLRMACTCCISKLEN-----LAMILDKDAW-----NK 753
DB 775 AVTRYEMKRGIVNDVVTSUKTAVVAAAAPFERNGLPTPKQLDMILVEXDSTEDND 834
QY 754 EEFVSLDELFTRSKVTFTVPKIFLLATSATLTERSEMKSTGLIDEVVIKPLRMSVLIC 813
DB 835 SEIRLLNSR-TNGNV-HHKSFKLALPATNITNSEFDRAKSAGFADTVIMKPLRSMIGAC 892
QY 814 LQFTLVNGKQRQPNRORN---LGHLLREKQIILVDDNLVNRVVAEGALKYGAIVTCVE 870
DB 893 LQOVLRLKTRQHPGSSPATLKSLLTGKILVDDNIVNRRVVAAGALKKFGAEVVCAC 952
QY 871 SGKAAALMLKPPHNFACFMDLQMPENDGFETARRVRELEREINKKTIASGEVAEMFCKF 930
DB 953 SGQVALGLQIPHTFACFMDIQMDGFETARRVRELEREINKKTIASGEVAEMFCKF 1000
QY 931 SSMHVPILAMTADVIQATHEECMKMGDGYVSKPFEEVLYTAVARFFEP 980
DB 1001 LEWHLPIAMTADVIHATVEECLKSGMDGYVSKPFEEENLYKSVAKSFKP 1050
RESULT 13
AAO22558
ID AAO22558 standard; Protein; 1057 AA.
XX
AC AAO22558;
XX
XX
DT 28-OCT-2002 (first entry)
DE
DE Wooden leg (WOL) gene related protein SEQ ID No 5.
XX
XX Wooden leg; WOL; vasculature; transgenic plant; agronomic; longer root;
XX wood production; plant; promoter; tree; crop plant.
XX Arabidopsis thaliana.
XX
XX WO200244337-A2.
XX
XX 06-JUN-2002.
XX
XX 29-NOV-2001; 2001WO-US45053.
XX
XX 29-NOV-2000; 2000US-253739P.
XX
XX (UYN) UNIV NEW YORK STATE.
PA (HELA/) HELARIUTTA Y.
PA (MAHO/) MAHONEN A P.
PA (BONK/) BONKE A W M.
PA (KAUP/) KAUPPINEN L.
PA (RIIK/) RIIKONEN M.
XX
XX Helariutta Y, Mahonen AP, Bonke AMW, Kauppinen L, Riiikonen M;
PI Benfey PN;
XX
XX WPI; 2002-599423/64.
XX
XX Novel isolated polypeptide (WOODEN LEG) with ability to regulate a set
PT of asymmetric cell divisions that establish vascular tissue in root and
PT hypocotyl development, useful for improving agronomically valuable
PT plants
XX
XX Claim 6; Fig 5D; 187pp; English.
XX
XX The invention relates to an isolated WOODEN LEG (WOL) polypeptide,
CC comprising 15 contiguous amino acids of a fully defined Arabidopsis
CC WOODEN LEG protein sequence of 1057 amino acids as given in the
CC specification, and to its encoding nucleic acid. The invention also
CC relates to an amino acid sequence of domains of protein, e.g., N-terminal
CC region, C-terminal domain, etc; or is a naturally occurring allelic
CC variant of the above mentioned polypeptide sequence. Expression levels of
CC the nucleic acid can be modified to improve the vasculature in transgenic
CC plants and enhance the agronomic properties of such plants. Also the WOL
CC promoter is used to drive expression of a heterologous coding sequence of

Db 89 GNKSGSTFTQERHALLPKAL-----ILWIIIVGFISSGIQWMDANK 131
QY 61 EIIMKRETLANCDERARVLQDFNVSLNHHVALSILVSTFHHGKIPSAIDQRTFEY 120
Db 132 ---IRREEVLVSMCDQARMQDFQSVNVHVALAILVSTFHHKPNPSAIDQETFAEY 188
QY 121 ERTNFERPLTSGVAYALKVPHSREKEFEKHGWAIKKMETEDQTVVQDCVPENFDPAP 180
Db 189 ARTAFERPLLSGVAYAEKVNVFERFERQHNVIKTM-----DRGEESPVR 235
QY 181 DEYAPVIFAQETVSHIVSDMSGEBEDRENILKARASGKVLTPPKLILKSNHILGVLT 240
Db 236 DEYAPVIFSDSVSYLESIDMSGEBEDRENILPARETGKAVLTPSPRLLETHHILGVLT 295
QY 241 AVYDTSLPDATEEQVEATIGYLGASDYMPSLVEKLLHQLASKQTIADVVDYDTTNTS 300
Db 296 PUYKSSLUPENPTVEERIAATAGYLGAFDVESLVENLLGQLAGNAQIAVVHVYDITNAS 355
QY 301 IKMYGS--EIGDISEOHISLIDFGDPSRNHEHCRPKHKLPWPWTAITPSILVLVIT 358
Db 356 LVNYGNODEADRSLSHESKLDGDPFRKHMTCRYHQKAPILNVLTTPVPLFFAIGFL 415
QY 359 GYILYBAINRIATVEEDCQMRLEKARABAAADIAKQFLATVSHSHEIRTPMNGVLGML 418
Db 416 GYILYGAAMHIIKVEDDFHEMQLKVRABEADVAKSQFLATVSHSHEIRTPMNGIL 475
QY 419 MDTDLDAKQMDYAQTANGSGKDLTSLINEVLDOAKIESGRLELENPFFDMRFILDNV 478
Db 476 LDTLSSTQDYAQTQAQVCKKALIALINEVLDRAKIEAGKLELESVPFDIRSILDDV 535
QY 479 LSGKANKEGIEGLAVVYSSQVDPVVGDPSRFRQIITNLVNSIKFTQERGHIFISV 538
Db 536 FSEESRNKSIELAVFVSDKVPEIVGDSGRFRQIITNLVNSIKFT--EKGHIFVKV 594
QY 539 EVK---EPL--TIRDAVLKQRLALGCSGESGTSGFPAVNAWGSWKNFKTCYSTES 593
Db 595 QSKDESEPKNALGVSEEMIVVSKQSYNTLSGYEADGRNSWDSFKHLVSEEQSLSE 654
QY 594 ---QIKLLVTVEDTGVGIPVDAQGRIFTPFMOADSTSTRTYGGTGIGLSISKRL 649
Db 655 DISSNVRLMVSIEDTGIGIPLVAQGRVFPFPMQADSSTSRNYGGTGIGLSISK 714
QY 650 GEMGFVSEPGISGTFSTFTGVFGKAEATNTSITKLER--FDLAIQETGLRALVID 707
Db 715 GQINFISRPHIGSTFTFTAVLEKDCRSAINHMKPNVEHLPSTFKGMKAIIVDA 774
QY 708 EVTRYELRIGISADIVSSLRMACTCCISKLEN-----LAMILIDKDAW----- 753
Db 775 AVTRYHMKRLGINVDVVTSLKTAVAAAFERNGSPPTKPOLDMILVEKDSWISTED 834
QY 754 EEPVSLDELFTRSKVTFTRVPKIFPLATSATLTERSEMKSGLIDEVWIKPLRMSV 813
Db 835 SEIRLINSR--TNGNV--HHKSPKLALPATNITNSEPDRAKSAGFADTVINKPLR 892
QY 814 LQETLVNGKKRQPNRQRN--LGHLLRKKQLIIVDDNLVNRVAVGALKKYKAI 870
Db 893 LQCVLELRKTRQOHPPGSSPATLKSLLTGKILVDDNINRRVAVGALKKFGAEV 952
QY 871 SGKAALAMLKPHNFACFMDLQMPEDMGDFEATRRVRELEREREINKKIASGEV 930
Db 953 SGQVALGLLQIPHITFACFMDIQMPQMDGFQATRQIRMMEKETKEKTN----- 1000
QY 931 SSWHPILAMTADVIOATHECMKCGMDGVVSKPFEVEVLYTAVARFPFP 960
Db 1001 LEWHLPIAMTADVIHATVEBCLKSGMDGVVSKPFEENLYKSAKSKFP 1050

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OM protein - protein search, using sw model

Run on: November 28, 2003, 14:02:30 ; Search time 27.7424 Seconds
(without alignments)
6681.678 Million cell updates/sec

Title: US-09-918-508-4_COPY_32_1036

Perfect score: 5159

Sequence: 1 GIEDKSGLLVGSVDLEKTK.....AEQLYREVSFFNPSPTES 1005

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 673684 seqs, 18443283 residues

Total number of hits satisfying chosen parameters: 673684

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Published Applications AA:*

- 1: /cgn2_6/ptodata/2/pubpaa/US07_PUBCOMB.pep.*
- 2: /cgn2_6/ptodata/2/pubpaa/PCT_NEW_PUB.pep.*
- 3: /cgn2_6/ptodata/2/pubpaa/US06_NEW_PUB.pep.*
- 4: /cgn2_6/ptodata/2/pubpaa/US06_PUBCOMB.pep.*
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- 9: /cgn2_6/ptodata/2/pubpaa/US09A_PUBCOMB.pep.*
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- 11: /cgn2_6/ptodata/2/pubpaa/US09C_PUBCOMB.pep.*
- 12: /cgn2_6/ptodata/2/pubpaa/US09_NEW_PUB.pep.*
- 13: /cgn2_6/ptodata/2/pubpaa/US10A_PUBCOMB.pep.*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	5159	100.0	1036	10 US-09-918-508-4	Sequence 4, Appli
2	5001	96.9	1092	14 US-10-135-322-18	Sequence 18, Appl
3	3389.5	65.7	1044	15 US-10-101-464A-956	Sequence 956, App
4	3385	65.6	1002	15 US-10-101-464A-957	Sequence 957, App
5	2806.5	54.4	1270	15 US-10-101-464A-979	Sequence 979, App
6	2685.5	52.1	1176	10 US-09-918-508-2	Sequence 2, Appli
7	2674	51.8	1173	14 US-10-135-322-19	Sequence 19, Appl
8	2585.5	50.1	997	15 US-10-101-464A-977	Sequence 977, App
9	2544.5	49.3	890	15 US-10-101-464A-958	Sequence 958, App
10	2481.5	48.1	1057	10 US-09-918-508-6	Sequence 6, Appli
11	2475.5	48.0	1057	14 US-10-135-322-5	Sequence 5, Appli
12	2475.5	48.0	1057	14 US-10-135-322-24	Sequence 24, Appli
13	2462	47.7	974	15 US-10-126-120-2	Sequence 2, Appli
14	1368.5	26.5	480	15 US-10-101-464A-978	Sequence 978, App
15	1041	20.2	482	15 US-10-101-464A-955	Sequence 955, App

16	975	18.9	412	15	US-10-101-464A-905	Sequence 905, App
17	937.5	18.2	426	15	US-10-101-464A-124	Sequence 124, App
18	867.5	16.8	274	14	US-10-135-322-8	Sequence 8, Appli
19	849.5	16.5	289	14	US-10-135-322-10	Sequence 10, Appli
20	651	12.6	1018	15	US-10-101-464A-909	Sequence 909, App
21	639.5	12.4	1081	10	US-09-424-951-4	Sequence 4, Appli
22	620	12.0	1447	15	US-10-156-761-8624	Sequence 8624, App
23	600	11.6	170	15	US-10-101-464A-116	Sequence 116, App
24	563	10.9	2150	14	US-10-135-322-17	Sequence 17, Appli
25	560	10.9	971	14	US-10-116-048-2	Sequence 2, Appli
26	560	10.9	2471	14	US-10-116-048-4	Sequence 4, Appli
27	557.5	10.8	1240	15	US-10-101-464A-976	Sequence 976, App
28	552	10.7	1829	15	US-10-156-761-10049	Sequence 10049, A
29	543	10.5	816	15	US-10-101-464A-827	Sequence 827, App
30	525.5	10.2	747	12	US-10-100-294A-27	Sequence 27, Appli
31	504	9.8	129	15	US-10-101-464A-828	Sequence 828, App
32	500	9.7	185	15	US-10-101-464A-822	Sequence 822, App
33	480.5	9.3	1383	15	US-10-156-761-13096	Sequence 13096, A
34	474.5	9.2	1220	10	US-09-801-368-332	Sequence 332, App
35	470.5	9.1	418	10	US-09-424-951-2	Sequence 2, Appli
36	462	9.0	123	14	US-10-135-322-12	Sequence 12, Appli
37	462	9.0	139	15	US-10-101-464A-820	Sequence 820, App
38	458.5	8.9	738	12	US-10-171-404A-36	Sequence 36, Appli
39	448	8.7	717	12	US-10-171-404A-38	Sequence 38, Appli
40	439.5	8.5	496	15	US-10-101-464A-906	Sequence 906, App
41	408.5	7.9	1373	12	US-10-032-585-7129	Sequence 7129, App
42	405	7.9	264	15	US-10-101-464A-959	Sequence 959, App
43	378.5	7.3	762	15	US-10-101-464A-114	Sequence 114, App
44	359	7.0	206	15	US-10-101-464A-120	Sequence 120, App
45	345.5	6.7	104	14	US-10-135-322-30	Sequence 30, Appli

ALIGNMENTS

RESULT 1

US-09-918-508-4
; Sequence 4, Application US/09918508
; Patent No. US20020177162A1
; GENERAL INFORMATION:
; APPLICANT: KAKIMOTO, TATSUO
; APPLICANT: HIGUCHI, MASAYUKI
; APPLICANT: INOUE, TSUTOMU
; TITLE OF INVENTION: ANALYSIS OF AGONIST-ACTIVITY AND ANTAGONIST-ACTIVITY
; TITLE OF INVENTION: TO CYTOKININ RECEPTOR
; FILE REFERENCE: Q65478
; CURRENT APPLICATION NUMBER: US/09/918,508
; PRIOR FILING DATE: 2001-08-01
; PRIOR APPLICATION NUMBER: JP 2001-073812
; PRIOR FILING DATE: 2001-03-15
; NUMBER OF SEQ ID NOS: 22
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 4
; LENGTH: 1036
; TYPE: PRT
; ORGANISM: Arabidopsis thaliana
US-09-918-508-4

Query Match 100.0%; Score 5159; DB 10; Length 1036;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1005; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db	32	GIEDKSGLLVGSVDLEKTKMTTLKKNKNMFWNKLSGSLKIPSFYQFLGSVKFNKAW	91
Qy	61	WRKLVVVVFWVLVSVTWTFWYFSSQAMEKXKKTSLASMCDEARMLODQFNVSNNHVOAM	120
Db	92	WRKLVVVVFWVLVSVTWTFWYFSSQAMEKXKKTSLASMCDEARMLODQFNVSNNHVOAM	151
Qy	121	SILISTFHGKIPSAIDQRTFSYTDRTSFERPLTSGVAYAMRVLHSEFEFERQCGWTI	180
Db	152	SILISTFHGKIPSAIDQRTFSYTDRTSFERPLTSGVAYAMRVLHSEFEFERQCGWTI	211

Qy	181	RKMYSLEONPVHKDYYDLEALEPSPVOBEYAPVIFAQDTVSHVVSJLMDLMSGKEDRENVL	241
Db	212	RKMYSLEONPVHKDYYDLEALEPSPVOBEYAPVIFAQDTVSHVVSJLMDLMSGKEDRENVL	271
Qy	241	ARSSGKGYLTAPFPLIKTNRLGVLITFAVYKRDLPNSNATPKERIEATNGYLGCVFDESJ	300
Db	272	ARSSGKGYLTAPFPLIKTNRLGVLITFAVYKRDLPNSNATPKERIEATNGYLGCVFDESJ	331
Qy	301	VENILLOQLASKOTILNVYVDITNHSQPSIMYCTNVSADGLERVSPLIFQDPIRKHEMR	360
Db	332	VENILLOQLASKOTILNVYVDITNHSQPSIMYCTNVSADGLERVSPLIFQDPIRKHEMR	391
Qy	361	FKQKPPWPVLSWMTSFGILVIALVAHIIHATVSRHKVBEEDCKMKQLKKKAEADVAK	420
Db	392	FKQKPPWPVLSWMTSFGILVIALVAHIIHATVSRHKVBEEDCKMKQLKKKAEADVAK	451
Qy	421	SQFLATVSHERTPMNGVLGMLHMLMDTDELDTVOQDYVYRTAQSGKALVSLINEVLDOAK	480
Db	452	SQFLATVSHERTPMNGVLGMLHMLMDTDELDTVOQDYVYRTAQSGKALVSLINEVLDOAK	511
Qy	481	IESGKLELEEVYRFDLRGILDDVLSFSSKSQKGVELAVIISDRVPDMLIGDPRPROIL	540
Db	512	IESGKLELEEVYRFDLRGILDDVLSFSSKSQKGVELAVIISDRVPDMLIGDPRPROIL	571
Qy	541	TNLMGNSIKFTEKGHIFVTVHLVDLFBESIDGETASSPESTISGLPVADRQSRWENFKAF	600
Db	572	TNLMGNSIKFTEKGHIFVTVHLVDLFBESIDGETASSPESTISGLPVADRQSRWENFKAF	631
Qy	601	SSNGHRSPEPPDDINLIVSVBEDTCGIPVEAQSRIFTPPMQVGPSSISSTHGGTGIGLSI	660
Db	632	SSNGHRSPEPPDDINLIVSVBEDTCGIPVEAQSRIFTPPMQVGPSSISSTHGGTGIGLSI	691
Qy	661	SKCLVGLMKGIIFSSTPKVGSFTFTTAVFSNGMQPAERKNDNNQPIFSEFRGMKAVVD	720
Db	692	SKCLVGLMKGIIFSSTPKVGSFTFTTAVFSNGMQPAERKNDNNQPIFSEFRGMKAVVD	751
Qy	721	HRPARAKVSWHFQBLGRVVEVPRVEQALHYLKITTTVMNMLIEQETWNRADDFIKK	780
Db	752	HRPARAKVSWHFQBLGRVVEVPRVEQALHYLKITTTVMNMLIEQETWNRADDFIKK	811
Qy	781	LQKDPLFISPKILLANSVSSISSEALCTGIDPPVIVKPLRASMALATLQRLGLGIGIRE	840
Db	812	LQKDPLFISPKILLANSVSSISSEALCTGIDPPVIVKPLRASMALATLQRLGLGIGIRE	871
Qy	841	PPQHKGPALILRNLLLGKILIVDDNNVNLVAAAGALKKYGADVVCVCAESGIKALSLEK	900
Db	872	PPQHKGPALILRNLLLGKILIVDDNNVNLVAAAGALKKYGADVVCVCAESGIKALSLEK	931
Qy	901	PHFEDACPMIDQMPMDGFEATRTRDMEEMWNKIKNGEALIVENGKNTSWEHLPVLAWT	960
Db	932	PHFEDACPMIDQMPMDGFEATRTRDMEEMWNKIKNGEALIVENGKNTSWEHLPVLAWT	991
Qy	961	ADVTQATHEECLKGMGDKVSKPFPAEOLYREVSRFFNPSDTE	1005
Db	992	ADVTQATHEECLKGMGDKVSKPFPAEOLYREVSRFFNPSDTE	1036

RESULT 2

[illegible]

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Qy 869 VNLRAAGALKKYGADVVCABSGIKATSLIKPPHEFDACFMIDIOPEMDGFEATRIRDM 928
Db 932 VNLRAAGALKKYGADVVCABSGIKATSLIKPPHEFDACFMIDIOPEMDGFEATRIRDM 991
Qy 929 EENMKRIKNGEALIVENGKTSWHLPLVAMTADVIQATHEECLKCGMDGY 979
Db 992 EENMKRIKNGEALIVENGKTSWHLPLVAMTADVIQATHEECLKCGMDGY 1042

RESULT 3
US-10-101-464A-956
; Sequence 956, Application US/10101464A
; Publication No. US20030046728A1
; GENERAL INFORMATION:
; APPLICANT: Strabala, Timothy
; APPLICANT: Nieuwenhuizen, Nicolaas
; APPLICANT: Higgins, Colleen M.
; TITLE OF INVENTION: Compositions Isolated from Plant Cells
; TITLE OF INVENTION: and Their Use in the Modification of Plant Cell Signaling
; FILE REFERENCE: 11000.1020c2
; CURRENT APPLICATION NUMBER: US/101/101.464A
; PRIOR FILING DATE: 2002-03-18
; PRIOR APPLICATION NUMBER: 09/704,302
; PRIOR FILING DATE: 2000-11-01
; PRIOR APPLICATION NUMBER: 09/228,986
; PRIOR FILING DATE: 1999-01-12
; PRIOR APPLICATION NUMBER: 60/162,866
; PRIOR FILING DATE: 1999-11-01
; PRIOR APPLICATION NUMBER: PCT/US00/00724
; PRIOR FILING DATE: 2000-01-11
; NUMBER OF SEQ ID NOS: 989
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 956
; LENGTH: 1044
; TYPE: PRT
; ORGANISM: Eucalyptus grandis
US-10-101-464A-956

Query Match 65.7%; Score 3389.5; DB 15; Length 1044;
Best Local Similarity 68.7%; Pred. No. 3.5e-297;
Matches 686; Conservative 97; Mismatches 194; Indels 21; Gaps 7;

Qy 17 EKTQMTTLKKNNKM--WFWNKISSGLKI-PSFSYQFLGSKVFNKAWRKLWVVVVVW 72
Db 38 EMTRAGELGDGKMSLNLW-EKVLGNVYKIHPSHNSQAGSKKFRKTWRRKVLWTWIGW 96
Qy 73 VLVSITWTFWYPSOAMERKKTSLASCDERARMLQDQFNVMNHHVQAMSLITFHHGKI 132
Db 97 FIISACIFWYMSQAASRRRTGLSMCDERARMLQDQFNVMNHHVQAMSLITFHHGKQ 156
Qy 133 PSAIDQRTFSYTDRTGFERPLTSGVAYAMEVLHSEEREPRQOGWTIRKMYSLQNPVH 192
Db 157 PSAIDQRTFYERTAFERPLTGFIAVAVLHCDREEFKAQGWKIKMDTVEKTPVH 216
Qy 193 KDDVDLBALEPSPVOEYAPVIFAQDTVSHVSLDMLSGKBDRENVLRARSSGKGVLTAP 252
Db 217 KONSELESPSPVOEYAPVIFAQDTIGHVVSLDMLSGKBDRENVLRARASGKGVLTAP 276
Qy 253 FPLIKTNRLGVLTFVYKRLPSNATPKERIEATNGVLGVFDIESLIVENLLQOLASKQ 312
Db 277 FRLIKTNSLGVILTFVYKRLPSNATPKERIEATNGVLGVFDIESLIVENLLQOLASKQ 336
Qy 313 TILVNVVDITNHSOPISMVGTNVSADGLERSPLIFGDLPLKHEMRCKRFKOPPPVPLSM 372
Db 337 NIVNVVDITNHSOPISMVGTNVSADGLERSPLIFGDLPLKHEMRCKRFKOPPPVPLSM 396
Qy 373 VTSFGILVIALVAHIIHATVSRIRKVEEDCDKMKQLKKAADAAVAKSQFLATVSHR 432
Db 397 TTSFGILVIALVGVIFQATVNRIAKVEDDVHKMKELKKRAADAAVAKSQFLATVSHR 456
Qy 433 TPMNGVLCMLHMLMDTDLDETQDYVYTAQESGKALVSLINEVLDQAKIESGKIEIAVQ 492
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Db 457 TPMNGVLCMLHMLMDTDLDETQDYVYTAQESGKALVSLINEVLDQAKIESGKIEIAVQ 516
Qy 493 FDLRGLDDVLSLFSKSKQOQVELAVYISDRVDPDMLIGDPRFRQILTNLMGNSIKFTE 552
Db 517 FDLRAILDDVLSLFSKSKQOQVELAVYISDRVDPDMLIGDPRFRQILTNLMGNSIKFTE 576
Qy 553 KGHIFVTVHLVDELFSIDGETASSPSTLSGLPVADQRORSWENFKAFSNGHRSPPFS- 611
Db 577 KGHILVTVHLVDELFSIDGETASSPSTLSGLPVADQRORSWENFKAFSNGHRSPPFS- 636
Qy 612 -PPDINLIVSDEDTGVGIPVEAQSRIPTPMQVGPISRTHGGTGIGLSISKLVGLMKG 670
Db 637 FSNPILNIIISVEDTGIGIPPEAQPRVTRPMQVGPISRTHGGTGIGLSISKLVGLMKG 696
Qy 671 EIGFSSTPKVGSTFTTFAVFSNGM-----QPAERKNDNNQPIFSEFRGMKAVVVDHR 722
Db 697 EIGFVSIPOVGSFTTFAVFDACSTSKCKGQOQVKGQDSGT--SEFHGMKALVVDTR 753
Qy 723 PARAKVSWYHFORLIGIRVEVPRVEQALHYLKTGTTVNMILLIBQETWNRD---DFIK 779
Db 754 FVRANVSKYHQRLIGHVEVADLNQCLHTIQSGNCRIDMWLLEWIEWDKDSGLSAIFLD 813
Qy 780 KLOKDXPLFLSKLILLANSVSEISALCTGIDPPIVIVKPLRASMLAATLQRCGLGIGIR 839
Db 814 KLKDMKRVSPRFLFLLSNSISSRMSGATTDTGPFVIMKPLRASMLVASFQRMVGVNR 873
Qy 840 EPPQHKGPALILRLNLLGRKILIVDDNNVNLRAAGALKKYGADVVCABSGIKATSLIK 899
Db 874 ISCSNGSPSLFLRNLLGRKILVDDNNVNLRAAGALKKYGADVVCABSGIKATSLIK 933
Qy 900 PPHFDACFMIDIOPEMDGFEATRIRDMEEENKRIKNGEALIVENGKTSWHLPLVAM 959
Db 934 PPHFDACFMIDIOPEMDGFEATRIRDMEEENKRIKNGEALIVENGKTSWHLPLVAM 993
Qy 960 TADVIQATHEECLKCGMDGYVYKPFPEAFOLYREVSREF 997
Db 994 TADVIQATHEECLKCGMDGYVYKPFPEAFOLYREVSREF 1031

RESULT 4
US-10-101-464A-957
; Sequence 957, Application US/10101464A
; Publication No. US20030046728A1
; GENERAL INFORMATION:
; APPLICANT: Strabala, Timothy
; APPLICANT: Nieuwenhuizen, Nicolaas
; APPLICANT: Higgins, Colleen M.
; TITLE OF INVENTION: Compositions Isolated from Plant Cells
; TITLE OF INVENTION: and Their Use in the Modification of Plant Cell Signaling
; FILE REFERENCE: 11000.1020c2
; CURRENT APPLICATION NUMBER: US/101/101.464A
; PRIOR FILING DATE: 2002-03-18
; PRIOR APPLICATION NUMBER: 09/704,302
; PRIOR FILING DATE: 2000-11-01
; PRIOR APPLICATION NUMBER: 09/228,986
; PRIOR FILING DATE: 1999-01-12
; PRIOR APPLICATION NUMBER: 60/162,866
; PRIOR FILING DATE: 1999-11-01
; PRIOR APPLICATION NUMBER: PCT/US00/00724
; PRIOR FILING DATE: 2000-01-11
; NUMBER OF SEQ ID NOS: 989
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 957
; LENGTH: 1002
; TYPE: PRT
; ORGANISM: Eucalyptus grandis
US-10-101-464A-957

Query Match 65.6%; Score 3385; DB 15; Length 1002;
Best Local Similarity 68.1%; Pred. No. 8.3e-297;
Matches 685; Conservative 115; Mismatches 182; Indels 24; Gaps 6;

Qy 2 IEDKSGLLVSGVDELEKTKMTTLKKNKMWFMNKRISSSGLKIPFSFYQLGSKVFNKAWW 61
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Db 1 MDAAKTGLGSD-----GKISLNWRDKVLGKIVKIQHQYDHLFGSKKISNALM 47
QY 62 RKLIVVVVFWVLVSIWTFWYSSQAMEKKETLASMCDERARMLDQFNVMNHHVQA 121
Db 48 RKLIVVFWCATWFLWISYMSQAIEKKETLASMCDERARMLDQFNVMNHHVQA 107
QY 122 ILISTFHGKIPSAIDQRTSEYTDRTSPERPLTSGVAYAMRVLHSEREFEFQQGWTIR 181
Db 108 ILISTFHGKIPSAIDQRTSEYTDRTSPERPLTSGVAYAMRVLHSEREFEFQQGWTIR 167
QY 182 KWSLEONPVHKDDYDLALEPSPVQEEYAPVIFAQDVTSHVVSIDMLSKGKEDRENVLRA 241
Db 168 RMDTLEQNVLHKDDYDLALEPSPVQEEYAPVIFAQDVTSHVVSIDMLSKGKEDRENVLRA 227
QY 242 RSSGKGVLTAPFPLIKTNRLGVLTFAVKYKDLPSNATPKERIEATNGVLGGVDFDIESIV 301
Db 228 RASGKGVLTAPFPLIKTNRLGVLTFAVKYKDLPSNATPKERIEATNGVLGGVDFDIESIV 287
QY 302 ENLLQOLASKQITLVNVDITNHSQIPISMYGTNVVSADGLERSVPLIFGDPPLRKHEMRCRF 361
Db 288 EKLLQOLASKQITLVNVDITNHSQIPISMYGTNVVSADGLERSVPLIFGDPPLRKHEMRCRF 347
QY 362 KOKPPEPVLVSWTSGFGLVIALIVAHIIHATVSRIRHKVEEDCDKMKQIKKABAAVAKS 421
Db 348 KOKPPEPVLVSWTSGFGLVIALIVAHIIHATVSRIRHKVEEDCDKMKQIKKABAAVAKS 407
QY 422 QFLATVSHERTPMNGVGLMHLMDTELDTQDVTQDYVVRTAQASGKALVSLINEVLDOAKI 481
Db 408 QFLATVSHERTPMNGVGLMHLMDTELDTQDVTQDYVVRTAQASGKALVSLINEVLDOAKI 467
QY 482 ESGKLELEVRFLRGILDDVLSFSSKQKQGVELAVVISDRVPOMLIGDPRFRQIIT 541
Db 468 ESGKLELEVRFLRGILDDVLSFSSKQKQGVELAVVISDRVPOMLIGDPRFRQIIT 527
QY 542 NLMGNSIKFTEKHIFVTVHLVDELPESIDGETASSPESTLSGLPVADRQORSWENFKAS 601
Db 528 NLMGNSIKFTEKHIFVTVHLVDELPESIDGETASSPESTLSGLPVADRQORSWENFKAS 587
QY 602 SNHG-RSFFPSPDP-INLIVSVDGTGVPVEAQSRIFTFPMQVGPSISRTHGGTGIGLS 659
Db 588 QHERVCSYSSYTDLNLIVSVDGTGVPVEAQSRIFTFPMQVGPSISRTHGGTGIGLS 647
QY 660 ISKCLVLMKGEIGFSTPKVGTFTFTAVFNSGMQ-----PAERKNDNNQPIFSEFRGM 714
Db 648 ISKCLVLMKGEIGFSTPKVGTFTFTAVFNSGMQ-----PAERKNDNNQPIFSEFRGM 707
QY 715 KAVVDHPRARAKVSYHFORLQIRVEVUPRVEQALHYLKI GTTVMNLLIEOEIWNREA 774
Db 708 SALVVDPRSRAKVSXHYHFORLQIRVEVUPRVEQALHYLKI GTTVMNLLIEOEIWNREA 767
QY 775 D---DRIKKLQKDPFLSPKILLANSVRESSISEALCTGIDDPVIVTKPLRASMLAATLQ 831
Db 768 DLSILFVDQLRHIDQKVTPLFLAKSISSTRSDNTVCTDHSFVIMKPLRASMLAATLQ 827
QY 832 RGLG-IGIREPPQKGPALILNRLGLKILIVDDNNVNLRAVAAGALKKYGADVVCBS 890
Db 828 RTNMGNMGNRYNANGEVSRSLQHLILGRKILIVDDNNVNLRAVAAGALKKYGADVVCBS 887
QY 891 GIKAISILKPPHFDACFMDIQMPEDMGFEATRIRIDMEEMMKRINKGEALLIENGNKT 950
Db 888 GKEAISILKPPHFDACFMDIQMPEDMGFEATRIRIDMEEMMKRINKGEALLIENGNKT 947
QY 951 SWHPLVMTADVIQATHEBCLCGMDGVVSKPFEABQLYREVSFRF 996
Db 948 NWHVPILMTADVIQATHEBCLCGMDGVVSKPFEABQLYREVSFRF 993
```

RESULT 5
US-10-101-464A-979
; Sequence 979, Application US/10101464A
; Publication No. US20030046728A1
; GENERAL INFORMATION:

```
; APPLICANT: Strabala, Timothy  
; APPLICANT: Nieuwenhuizen, Nicolaas  
; APPLICANT: Higgins, Colleen M.  
; TITLE OF INVENTION: Compositions Isolated from Plant Cells  
; TITLE OF INVENTION: and Their Use in the Modification of Plant Cell Signaling  
; FILE REFERENCE: 11000.1020C2  
; CURRENT APPLICATION NUMBER: US/10/101,464A  
; CURRENT FILING DATE: 2002-03-18  
; PRIOR APPLICATION NUMBER: 09/704,302  
; PRIOR FILING DATE: 2000-11-01  
; PRIOR APPLICATION NUMBER: 09/228,986  
; PRIOR FILING DATE: 1999-01-12  
; PRIOR APPLICATION NUMBER: 60/162,866  
; PRIOR FILING DATE: 1999-11-01  
; PRIOR APPLICATION NUMBER: PCT/US00/00724  
; PRIOR FILING DATE: 2000-01-11  
; NUMBER OF SEQ ID NOS: 989  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 979  
; LENGTH: 1270  
; TYPE: PRN  
; ORGANISM: Eucalyptus grandis  
; US-10-101-464A-979  
  
Query Match 54.4%; Score 2806.5; DB 15; Length 1270;  
Best Local Similarity 58.8%; Pred. No. 3e-244;  
Matches 570; Conservative 148; Mismatches 212; Indels 39; Gaps 11;  
  
QY 60 WRRKLVVVVFWVLVSIWTFWYSSQAMEKKETLASMCDERARMLDQFNVMNHHVQA 119  
Db 311 WRRKLVVVVFWVLVSIWTFWYSSQAMEKKETLASMCDERARMLDQFNVMNHHVQA 370  
QY 120 MSILISTFHGKIPSAIDQRTSEYTDRTSPERPLTSGVAYAMRVLHSEREFEFQQGWT 179  
Db 371 LAILVSTFHGKIPSAIDQRTSEYTDRTSPERPLTSGVAYAMRVLHSEREFEFQQGWT 430  
QY 180 IRKMYSLQONPVHKDDYDLALEPSPVQEEYAPVIFAQDVTSHVVSIDMLSKGKEDRENVL 239  
Db 431 IKKMETADQTLV--PDYMLDRLDPAIQDEYAPVVSQETVSHVISIDMMSGKEDRENIL 488  
QY 240 RARSCKGVLTAFFPLIKTNRLGVLTFAVKYKDLPSNATPKERIEATNGVLGGVDFDIES 299  
Db 489 RARSCKGVLTAFFPLIKTNRLGVLTFAVKYKDLPSNATPKERIEATNGVLGGVDFDIES 548  
QY 300 LVENLLQOLASKQITLVNVDITNHSQIPISMYGTNVVSADGLERSVPLIFGDPPLRKHEMRC 359  
Db 549 LVEKLLHQLASKQITLVNVDITNHSQIPISMYGTNVVSADGLERSVPLIFGDPPLRKHEMRC 608  
QY 360 RPKQPPVPLVSWTSGFGLVIALIVAHIIHATVSRIRHKVEEDCDKMKQIKKABAAVAKS 419  
Db 609 RPKQPPVPLVSWTSGFGLVIALIVAHIIHATVSRIRHKVEEDCDKMKQIKKABAAVAKS 668  
QY 420 KSQFLATVSHERTPMNGVGLMHLMDTELDTQDVTQDYVVRTAQASGKALVSLINEVLDOA 479  
Db 669 KSQFLATVSHERTPMNGVGLMHLMDTELDTQDVTQDYVVRTAQASGKALVSLINEVLDOA 728  
QY 480 KTESGKLELEVRFLRGILDDVLSFSSKQKQGVELAVVISDRVPOMLIGDPRFRQI 539  
Db 729 KTESGKLELEVRFLRGILDDVLSFSSKQKQGVELAVVISDRVPOMLIGDPRFRQI 788  
QY 540 LTNMGNSIKFTEKHIFVTVHLVDE-----LFESIDGETASSPESTLSGLP 586  
Db 789 LTNMGNSIKFTEKHIFVTVHLVDE-----LFESIDGETASSPESTLSGLP 848  
QY 587 VADRORSWENFKASISKCLVLMKGEIGFSTPKVGTFTFTAVFNSGMQ-----PAERKNDNNQ 705  
Db 906 TSRTTGGTGIGLSISKCLVLMKGEIGFSTPKVGTFTFTAVFNSGMQ-----PAERKNDNNQ 965  
QY 706 PTFSEFRGMKAVVVDHPRARAKVSYHFORLQIRVEVUPRVEQALHYLKI GTTVMNLLIEOEIWNREA 760
```

Db 966 SILEPGLRALVIDKXHIRAEVARYHLERIRISVDVACSLKSACTVLSNSSPREISDF 1025
Qy 761 NMILIEQIMNREAD-----DFIKLQ--KDPLFSPKLILLANSVSSISEA---LCTG 810
Db 1026 DMVLIDKVDMDRQGLNELNISLWKHRQNGSVSRPKFIPLATSI-SPIEHSSELKLANL 1084
Qy 811 IDPPIVIVKPLRASMLAATLQRGIGIGIREPPQHKGPALLIRNLLGRKTLIVDDNNVN 870
Db 1085 VDN--VIAKPLURLSVLISFLOEALNGKGRKLSRDR--KVSTLGLSKRRILVVDDNLVN 1140
Qy 871 LRVAAGALKKYGADVCAESGKAIKSLKPPHEFDACFMDIQMPMDGFEATRIRIDWEE 930
Db 1141 RRVAEGLKKGAIKGYVTCVSGKDAVAKLOPHDPAACFMDIQMPMDGFEATRIRHLES 1200
Qy 931 BMNRIKNGEALIVENGKNTSWHLPLVLAWTADVIQATHEECLKCGMDGYVSKPFEABOLY 990
Db 1201 EVNSKIASGEVSSDAFQNVVHHTPIANTADVIQATNEECLKCGMDGYVSKPFEABOLY 1260
Qy 991 REVSRFFNS 999
Db 1261 SAVARFFES 1269
RESULT 6
US-09-918-508-2
; Sequence 2, Application US/09918508
; Patent No. US20020177162A1
; GENERAL INFORMATION:
; APPLICANT: KAKIMOTO, TATSUO
; APPLICANT: HIGUCHI, MASAYUKI
; APPLICANT: INOUE, TSUTOMU
; TITLE OF INVENTION: ANALYSIS OF AGONIST-ACTIVITY AND ANTAGONIST-ACTIVITY
; TITLE OF INVENTION: TO CYTOKININ RECEPTOR
; FILE REFERENCE: Q65478
; CURRENT APPLICATION NUMBER: US/09/918,508
; CURRENT FILING DATE: 2001-08-01
; PRIOR APPLICATION NUMBER: JP 2001-073812
; PRIOR FILING DATE: 2001-03-15
; NUMBER OF SEQ ID NOS: 22
; SOFTWARE: Patent In Ver. 2.1
; SEQ ID NO 2
; LENGTH: 1176
; TYPE: PRF
; ORGANISM: Arabidopsis thaliana
US-09-918-508-2

Query Match 52.1%; Score 2685.5; DB 10; Length 1176;
Best Local Similarity 57.2%; Pred. No. 2.4e-233;
Matches 551; Conservative 142; Mismatches 224; Indels 47; Gaps 13;
Qy 61 WRK-LVVVVVFWVLVSIWTFWYFSSQAMEKRRKKTLSMCDERARMLQDQPNVSMNHVQA 119
Db 230 WRKNILLGILGVSFVSFWFMDTNEEIMKRRTLANMCDERARVLQDQPNVSLNHVA 289
Qy 120 MSILISTPHKIPISADQRTFSYRTSRLTSGVAYAMVLSHREPRQOGWT 179
Db 290 LSILVSTPHKIPISADQRTFSYRTSRLTSGVAYALKVPHSERKFEKGWA 349
Qy 180 IRKMYLEQNPVHKDDYDLRALESPVQEEYAPVIFAQDTSVHVSLDMLSGKEDRENVL 239
Db 350 IKOMETEDQTVV--QDCVPENFDPAQIQDEYAPVIFAQETVSHVSVDMMSGEDRENIL 407
Qy 240 RARSNGKVLTPAPPLIKTNRLGLVITFAYVKRDLPSNATPKERIEATNGYLGGVFIDIES 299
Db 408 RARSNGKVLTPSPFKLLKSNHGLVITFAVYDTSLPDPDATEEQRVATEIGVLAGSYDMP 467
Qy 300 LVENLLQOLASKOILVNVYDITHSQPISWYGNVNSADGLRVSPLIFGDLPKHEMRC 359
Db 468 LVEKLLHQLASKOTIADVYDTTNTSLGIKMYGSEIGDISRQHTSSLDGDPDSNHEMHC 527
Qy 360 RFKOKPWPVLSMTYSGILVIALVAHIHATVSRHVKVEEDCDKMKLKKAEADVA 419

Db 528 RFXHKLPIPWTAITPSTILVLVITPLVGYIIEAINRIATVEEDCQKRELKARAEADIA 587
Qy 420 KSQFLATVSHIETPPMNGVLGMHLMDLTDLVQQDYVTRTAQASGKALVSLINEVLDOA 479
Db 588 KSQFLATVSHIETPPMNGVLGMHLMDLTDLDAQMDYAQYTAHSGKDLTSLINEVLDOA 647
Qy 480 KIESGKLELEVEFDLIGILDDVLSTFSSKQOKGVELAVYISDRVDMILIGDPRPROI 539
Db 648 KIESGRLELNVPPDMRFDILDNVSSLSGRANKEIGELAVYVSSQVDPVVVDPSRPROI 707
Qy 540 LTNLMGNSIKFT-EKGHIFVTVHLVDELFSIDGETA-----SSPESTLSGLPVA 588
Db 708 ITNLVGNISIKFTQERGHIFISVHLADVEKPELTIEDAVLQRLALGCSSESGETVSGPAV 767
Qy 589 DRQSWENFK-APSSNGHRSEFSPDPDINILVSVEDTGVGIPVBAQSRITTPRMQVGEI 647
Db 768 NAMGWNKFTCYSTESQNS-----DQIKLLVTVEDTGVGIPVDAQGRIFTTPFMQADSST 822
Qy 648 SRTHGGTGIGLSISKCLVGLMKGEIGFSPSTPKYGSTFTTAVFSNGMQPAERKNDNQPI 707
Db 823 SRTYGGTGIGLSISKRLVLMQGEIMGVSEFGIGSTFSTGVFG-----KAETNTSI 874
Qy 708 -----FSEFRGMKAVVDHRPARAKVSWYHFORLIGIRVWVPRVQALHYLKITGT 758
Db 875 TKLERFDLAIQETGLREALVIDNENIRAEVTRVELRLGISADIVSSLRVACTCCISKLE 934
Qy 759 TVNMILIEQIMNREADDFIKL---OKDFLSPKLILLANSVE-SSISEALCTG-IDP 813
Db 935 NLAMILIDKDAWNKEEFSVLDELFTRSKVTFTRVPKIFLLATSATLTERSEMSTGLIDE 994
Qy 814 PIVIVELRASMLAATLQRGIGIGIREPPQHKGPALLIRNLLGRKTLIVDDNNVLV 873
Db 995 --VWIKPLRMSVLICQETLVNKKRQPNRQ---RRNLGHLRBEKQILVVDNVLNRRV 1049
Qy 874 AAGALKKYGADVCAESGKAIKSLKPPHEFDACFMDIQMPMDGFEATRIRIDWEEBN 933
Db 1050 AEGALKKYGAIVTCVSGKAAALAMLPKPHNFDACFMDIQMPMDGFEATRIRVRELEIN 1109
Qy 934 KRINGEALIVENGKNTSWHLPLVLAWTADVIQATHEECLKCGMDGYVSKPFEABOLY 993
Db 1110 KKIAGSVSAEMFCFSSWHVPILAMTADVIQATHEECLKCGMDGYVSKPFEABOLY 1169
Qy 994 SRF 997
Db 1170 ARPF 1173
RESULT 7
US-10-135-322-19
; Sequence 19, Application US/10135322
; Publication No. US20020173017A1
; GENERAL INFORMATION:
; APPLICANT: BENFEY, PN
; APPLICANT: HELARIUTTA, Y
; APPLICANT: MAHONEN, AP
; APPLICANT: BONKE, AMW
; APPLICANT: KAUPPINEN, L
; APPLICANT: RIIKONEN, M
; TITLE OF INVENTION: WOODEN LEG GENE, PROMOTER AND USES THEREOF
; FILE REFERENCE: 5914-086-999
; CURRENT APPLICATION NUMBER: US/10/135,322
; CURRENT FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: 60/253,739
; PRIOR FILING DATE: 2000-11-29
; NUMBER OF SEQ ID NOS: 43
; SOFTWARE: Patent In version 3.0
; SEQ ID NO 19
; LENGTH: 1173
; TYPE: PRF
; ORGANISM: Arabidopsis thaliana
US-10-135-322-19

Query Match

51.8%; Score 2674; DB 14; Length 1173;

Best Local Similarity 57.0%; Pred. No. 2.6e-232;
Matches 549; Conservative 142; Mismatches 224; Indels 48; Gaps 13;

QY 61 WRX-LVVVVVFWVLVSITWTFYSSQAMEKREKKTETIASMCDERARMLQDFVNMHVQA 119
Db 230 WRKNILLGLGCVSFWFMDTNEIIMKRETLANNCDERARVLQDFVNSLVHVA 289

QY 120 MSLLSTFHGKIPSAIDORTSEYTDRTSFRPLTSGVAYAMRVLSRERFEROQGW 179
Db 290 LSLVSTFHGKIPSAIDORTSEYTDRTSFRPLTSGVAYAMRVLSRERFEROQGW 349

QY 180 IRKMYLEQNPVHKDDYDLEALPSPVQREYAPVIFAQDTVSHVSLDMLSGKEDRENVL 239
Db 350 IKOMETEDQTV--QDCVENFDPAIQEYAPVIFAQDTVSHVSLDMLSGKEDRENVL 407

QY 240 RARSSKGVLTAFFPLIKNRLGVLITFAVYKRDLPSPNATPKERIBATNGYLGGVFDIBS 299
Db 408 RARSSKGVLTAFFPLIKNRLGVLITFAVYKRDLPSPNATPKERIBATNGYLGGVFDIBS 467

QY 300 LVENILQOLASKOTILVNYVDITNHSQPISMWGTNVSADGLERVSPLIFGDPRLKHEMRC 359
Db 468 LVEKLLHQALASKOTIADVVDYDTNTSGLIKMYGSEIGDISQHISSLDLDFGDPSSRHEMHC 527

QY 360 RPKQKPPVPLSMVTSFGILVIALVAHIIHATVSRHKVBERCDKMKOLKKKARAADVA 419
Db 528 RPKKLPPIPTWALTPTSLVITFLVGYLYEAINRIATVEEDCQKRELKARAEADIA 587

QY 420 KSQFLATVSHETPMPNGVLGMLHMLMDTELDTVQDYVYRTAQASGKALVSLINEVLDQA 479
Db 588 KSQFLATVSHETPMPNGVLGMLHMLMDTELDTVQDYVYRTAQASGKALVSLINEVLDQA 647

QY 480 KIESGKLEBEYRFDLGRILDVLSFSSKQOKGVELAVYISDRVPMMLIGDGRFRQI 539
Db 648 KIESGKLEBEYRFDLGRILDVLSFSSKQOKGVELAVYISDRVPMMLIGDGRFRQI 707

QY 540 LTNLMGNSIKFTEKGIHIVTVHLVDELFSIDGTA-----SSPESTLSGLPVAD 589
Db 708 LTNLMGNSIKFTEKGIHIVTVHLVDELFSIDGTA-----SSPESTLSGLPVAD 765

QY 590 RQRWENFX-AFSSNGHRFEPSPDPINLIVSEDTGVGIPVEAQSRIFTPFQWGPSTIS 648
Db 766 ANGSKNFKTCYSTESQNS-----DQIKLLVITVEDTGVGIPVDAQRIFTFPWQADSSTS 820

QY 649 RTHGGTGIGLSISKVLGMLKGEIGFSSPTKVGSTPTFTAVFSNGNQPAERKNDNNQPI- 707
Db 821 RTHGGTGIGLSISKVLGMLKGEIGFSSPTKVGSTPTFTAVFSNGNQPAERKNDNNQPI- 872

QY 708 -----FSEPRGMKAVVDHPRAPAKVSWYHFORLGRVVRVVEQALHVLKIGTTT 759
Db 873 KLRFDLAIQEFGLRALVIDNRIAREVTRVELRLGSIADIVSSLRWACTCCISKLEN 932

QY 760 VNMILIEQBIWREADDFFIKGL---OKPLFSPKLILIANVSE-SSISEALCTG-IDPP 814
Db 933 LAMILIDKAWNKEBPSVLDLFTRSKVTFTVPKIFLLATSATLTERSEMSTGLIDE- 991

QY 815 IVIVPLRASMALAAITQRLGIGIREPPQHKGPALILNLLGRKILIVDNNVNLRA 874
Db 992 -VVIVPLRASMALAAITQRLGIGIREPPQHKGPALILNLLGRKILIVDNNVNLRA 1047

QY 875 AGALKYKADVVCAESGKAIKILKPPHSEFACFMDIOMPENMDGPEATRIEMEEENK 934
Db 1048 EGALKYKAIKILKPPHSEFACFMDIOMPENMDGPEATRIEMEEENK 1107

QY 935 RINKNGEALIVENGKTSWHLPLVAMTADVIQATHEECLKCGMDGYVSKPFEAEQIYREVS 994
Db 1108 KIASGEVSAEMFCKFSSWHVPLAMTADVIQATHEECLKCGMDGYVSKPFEAEQIYREVS 1167

QY 995 RFF 997
Db 1168 RFF 1170

US-10-101-464A-977
; Sequence 977, Application US/10101464A
; Publication No. US20030046728A1
; GENERAL INFORMATION:
; APPLICANT: Strabala, Timothy
; APPLICANT: Nieuwenhuizen, Nicolaas
; APPLICANT: Higgins, Colleen M.
; TITLE OF INVENTION: Compositions Isolated from Plant Cells
; TITLE OF INVENTION: and Their Use in the Modification of Plant Cell Signaling
; FILE REFERENCE: 11000.1020C2
; CURRENT APPLICATION NUMBER: US/10/101,464A
; PRIORITY FILING DATE: 2002-03-18
; PRIOR APPLICATION NUMBER: 09/704,302
; PRIOR FILING DATE: 2000-11-01
; PRIOR APPLICATION NUMBER: 09/228,986
; PRIOR FILING DATE: 1999-01-12
; PRIOR APPLICATION NUMBER: 60/162,866
; PRIOR FILING DATE: 1999-11-01
; PRIOR APPLICATION NUMBER: PCT/US00/00724
; PRIOR FILING DATE: 2000-01-11
; NUMBER OF SEQ ID NOS: 989
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 977
; LENGTH: 997
; TYPE: PRT
; ORGANISM: Eucalyptus grandis
US-10-101-464A-977

Query Match 50.1%; Score 2585.5; DB 15; Length 997;
Best Local Similarity 53.8%; Pred. No. 2.1e-224;
Matches 536; Conservative 160; Mismatches 228; Indels 73; Gaps 14;

QY 48 YQFLSGVFNKAWRKLVVVVVFWVLVSITWTFYSSQAMEKREKKTETIASMCDERARMLQ 107
Db 26 YTFIQS---NRAWIPKILVSVGMAFLSMISYRKWDADIKVRKEVLVSMCDQARMK 82

QY 108 DQFNVSMMHVQAMSLISTFHGKIPSAIDORTSEYTDRTSFRPLTSGVAYAMRVLSH 167
Db 83 DQFNVSMMHVQAMSLISTFHGKIPSAIDORTSEYTDRTSFRPLTSGVAYAMRVLSH 142

QY 168 RREPEROQGWITRKMYSLQNPVHKDDYDLEALPSPVQREYAPVIFAQDTVSHVSLD 227
Db 143 RREPEROQGWITRKMYSLQNPVHKDDYDLEALPSPVQREYAPVIFAQDTVSHVSLD 186

QY 228 MLSGKEDRENVLARSSKGVLTAFFPLIKNRLGVLITFAVYKRDLPSPNATPKERIBAT 287
Db 187 MMSGEEDRENILARATCKAVLTSPFLLGSHHLGVLTFFVYKSLPNTVPERIEAT 246

QY 288 NGYLGGVFEDISLVENILQOLASKOTILVNYVDITNHSQPISMWGTNVS--DGLERVSP 345
Db 247 VGYLGGAFFVESLVENILQOLASKOTILVNYVDITNHSQPISMWGTNVS--DGLERVSP 306

QY 346 LIFGDLPLKHEMRCRFPKPPVPLSMVTSFGILVIALVAHIIHATVSRHKVBERCDK 405
Db 307 LDFGDLPLKHEMRCRFPKPPVPLSMVTSFGILVIALVAHIIHATVSRHKVBERCDK 366

QY 406 MKQLKKAEADVAQSKQFLATVSHETPMPNGVLGMLHMLMDTELDTVQDYVYRTAQASG 465
Db 367 MQELKVAEADVAQSKQFLATVSHETPMPNGVLGMLHMLMDTELDTVQDYVYRTAQASG 426

QY 466 KALVSLINEVLDQAKIESGKLEBEYRFDLGRILDVLSFSSKQOKGVELAVYISDRV 525
Db 427 KALVSLINEVLDQAKIESGKLEBEYRFDLGRILDVLSFSSKQOKGVELAVYISDRV 486

QY 526 PDMILGDPGRFQILTNLMGNSIKFTEKGIHIVTVHLVDELFSIDGTA-----SPE-- 579
Db 487 PEIVMGDPGRFQILTNLMGNSIKFTEKGIHIVTVHLVDELFSIDGTA-----SPE-- 546

QY 580 -----STLSGLPVADROKSWENFKAF-----SSNGHRFEPSPDPINLIVSVED 623
Db 547 ILISDGSQLETLSCGEVADERSNDTFLNLLVAEQFNSVDNMTSNSEASENTVNVSVED 606

QY 624 TVGVIPVBAQSRIFTPFQWGPSTISRTHGGTGIGLSISKVLGMLKGEIGFSSPTKVGST 683

Db 607 TGIGIPLAQRVFPFMOADSSTRTYGGTIGLISISKCLVELMGHINIFISPOIGST 666
Qy 684 FTFAVFNQMGQPAERKNDNN-----QPIFSEFRGMKAVVVDHRRPARAKVSWYHFQRLGI 738
Db 667 PSFTAVFGR-----CKRLVFANVKRTFEDLPQGFGLKALVVDGKPVRAAVTRYHLNRLGI 722
Qy 739 RVEUVPVREQAL-----HYLKIGITTYTVMILIEQBIWNREADDFIKKL-----QKDLF 787
Db 723 NVEVASSNATATGCKNGSITAGYRHPDIILVEKDDMMSSIDSISUTVADWKQNGNLI 782
Qy 788 LSPKLILILANGSESSISALCTGDPPIVIVKPLRASMLAATLQRLGIGIGIREPPO----- 843
Db 783 QLPKILLASKISASELEKASGP-ADTVINKPVRASMLAALCQVIGIGIRKKQLQKQDMN 841
Qy 844 -HKGPAPILILNLLGRKILVDDNNVNLRAAGALKYKYGADVVCAESGIGIKAIISILKPPH 902
Db 842 MRNGSSA--LRSLLYGKILVDDNKVNRVAAGALKKFGANVECAESGKAALQLLPH 899
Qy 903 EFDACFMDIOMPMDGFEATRIRDMEMEMKRIKNGEALLIVENGKTSWHLPLVAMTAD 962
Db 900 DFDACFMDIOMPMDGFEATRIRDMESQVNEQMKSESAGQIVRGGE--WHMPTLAMTAD 957
Qy 963 VIQATHEBECLKGMDGVYKPFPAEOLYREYSRPFNS 999
Db 958 VIHATYDECLKGMGDGVYKPFDEENLYQAVAKFRT 994

RESULT 9

US-10-101-464A-958
; Sequence 958, Application US/10101464A
; Publication No. US20030046728A1
; GENERAL INFORMATION:
; APPLICANT: Strabala, Timothy
; APPLICANT: Nieuwenhuizen, Nicolaas
; APPLICANT: Higgins, Colleen M.
; TITLE OF INVENTION: Compositions Isolated from Plant Cells
; TITLE OF INVENTION: and Their Use in the Modification of Plant Cell Signaling
; FILE REFERENCE: 11000.1020c2
; CURRENT APPLICATION NUMBER: US/10/101.464A
; CURRENT FILING DATE: 2002-03-18
; PRIOR APPLICATION NUMBER: 09/704,302
; PRIOR FILING DATE: 2000-11-01
; PRIOR APPLICATION NUMBER: 09/228,986
; PRIOR FILING DATE: 1999-01-12
; PRIOR APPLICATION NUMBER: 60/162,866
; PRIOR FILING DATE: 1999-11-01
; PRIOR APPLICATION NUMBER: PCT/US00/00724
; PRIOR FILING DATE: 2000-01-11
; NUMBER OF SEQ ID NOS: 989
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 958
; LENGTH: 890
; TYPE: PRT
; ORGANISM: Eucalyptus grandis
US-10-101-464A-958

Query Match 49.3%; Score 2544.5; DB 15; Length 890;
Best Local Similarity 58.4%; Pred. No. 8.7e-221;
Matches 523; Conservative 133; Mismatches 201; Indels 39; Gaps 11;

Qy 133 PSAIDQTFSEYTRTFRPLTSGVAYAMVLSHREEREFROQGWTRKXYSLEQNPVH 192
Db 4 PSAIDQTFSEYTRTFRPLTSGVAYALVPHSRESEFEKRDHWTIKKMETADQTLV- 62
Qy 193 KDDYDLAALBSPVOEYAPVIFQADTVSHVVSIDMLSKEDRENVLRARSSKGVLTAP 252
Db 63 -PDYMLDRLOPAPIQDEYAPVVFQSETVSHVSDMMSKEDRENILRARASGKGVLTSP 121
Qy 253 FPLIKTNRLGVILTFVAVKRLPLGNATPKERIEATNGVLGGVDFIESLVNLLQOLASKQ 312
Db 122 FKLLKSNHLGVILTFVAVYDRELPAATAQRIEATVGLGASVDVPSLVEKLHLQOLASKQ 181

Qy 313 TILNVYDITNHSOPISMYGTNVISADGLERVSPLIFGDPLEKHEMRCKPKQPPWPVLSM 372
Db 182 TIVNVYDITNHSOPISMYGTNVISADGLERVSPLIFGDPLEKHEMRCKPKQPPWPVLSM 241
Qy 373 VTSFGILVIALVAHIHATVSRTHKVEEDCKMKQKKAADAAVAKSOPLATVSHR 432
Db 242 NSSVGLVITLVLVGHIFHAIINRIAKVEEDYROMMELKRAEAAADVAKSOPLATVSHR 301
Qy 433 TPMNGVGLMLHMLMDTDLTDYQVYRTAQASGKALVSLINEVLDQAKISGKLEBEVR 492
Db 302 TPMNGVGLMLQMLMDTNLANQLDYQATAHACGKDLISLINEVLDQAKISGKLEBEVR 361
Qy 493 FDLRGILDDVLSPESSKQKQVGLAVYISDRVDPMLIGDPRFRQILTNLMGNSIKPTE 552
Db 362 FDLRLALDNVLSITSGRSNEKGIELAVYSDRVPEAVIGDPRFRQIITNLVGNISIKPTH 421
Qy 553 KGHIFVTVHLVDE-----LFESIDGTASSPESTLSGLVADQRORSEWPKA 599
Db 422 EGHIFVSVHLLBEGCSQHDPRDVEKRLSSNLVEDTSKTFNTLSGQVVDRRKSWERPKK 481
Qy 600 FSSNGHRSFPSPDPINLIYSVEDTGVGIPEAQSRIFTFPMQVGPISIRTHGCTGIGLS 659
Db 482 LNRSDQIDVNES---VEVLVTVEDTGVGIAREAGSRIFTFVQADSTSTRTYGGTIGLS 538
Qy 660 ISKCLVGLMKEIGFSPSTPKVGTFTTAVFSN-GMOPABRKNDNNQPIFSEFPGMKAVV 718
Db 539 ISKCLVGLMKEIGFVSEPGTSTFTVPFAKEMNCLEVKQNYDSIISSEFAGLRALV 598
Qy 719 VDRPARAKVSWYHFQRLGIRVEVPRVEQALHVKIGT-----TIVNMLIEQEIWNRE 773
Db 599 IDKRIHRAEVARVHLERLRSVDVACLSKACTVLSNSSSPRELSDPMDVLIDKQVMDRQ 658
Qy 774 AD-----DFIKKLQ--KDPLFLSPKLILANSVSESSISEA---LCTGIDPPIVVKPLRA 823
Db 659 TGLELNLISLWKHRQNGSVSIRPKIFLATSI-SPIESELKLANLVDN--VLAKPLRL 715
Qy 824 SMLAATLQRLGIGTIGIREPPHOKGPPALILNLLGRKILVDDNNVNLRAAGALKYKA 883
Db 716 SVLISFLQELGALNGKRLSDRR--KVSTGLSKLGRILVDDNVLNRRVAEGALKYKA 773
Qy 884 DVVCAESGIIKAIISLKPHEFDFACFMDIOMPMDGFEATRIRDMEMEMKRIKNGEALI 943
Db 774 IVTCVSGKDAVAKLQPPHDFACFMDIOMPMDGFEATRIRHLESEVNSKIASGEVSS 833
Qy 944 VENGNKTSWHLPLVAMTADVIQATHEBECLKGMDGVYKPFPAEOLYREYSRPFNS 999
Db 834 DAFQNVVHHTPILAMTADVIQATNEBECLKGMDGVYKPFPAEOLYREYSRPFNS 889

RESULT 10

US-09-918-508-6
; Sequence 6, Application US/09918508
; Patent No. US20020177162A1
; GENERAL INFORMATION:
; APPLICANT: KAKIMOTO, TATSUO
; APPLICANT: HIGUCHI, MASAYUKI
; APPLICANT: INOUE, TSUTOMU
; TITLE OF INVENTION: ANALYSIS OF AGONIST-ACTIVITY AND ANTAGONIST-ACTIVITY
; TITLE OF INVENTION: TO CYTOKININ RECEPTOR
; FILE REFERENCE: 065478
; CURRENT APPLICATION NUMBER: US/09/918,508
; CURRENT FILING DATE: 2001-08-01
; PRIOR APPLICATION NUMBER: JP 2001-073812
; PRIOR FILING DATE: 2001-03-15
; NUMBER OF SEQ ID NOS: 22
; SOFTWARE: Patent in Ver. 2.1
; SEQ ID NO 6
; LENGTH: 1057
; TYPE: PRT
; ORGANISM: Arabidopsis thaliana
US-09-918-508-6

Query Match 48.1%; Score 2481.5; DB 10; Length 1057;

Db 622 SYNTLSGYEADGRNSWDFKHLVSEESQSLSEFDS-SNRLMWSIEDTGIGIPLVAQGR 680
Qy 636 IFTPMQVGPISRTHTGGTIGLSISKCLVGLMKGEIGFSSTPKVGSFTFTAVFS---- 691
Db 681 VFMPFQADSSSTRNYGGTIGLSISKCLVGLMRGQINFISRPHIGSTFTFTAVLEKCDK 740
Qy 692 ---NGMQPAERKNDNQPISEFRCMKAVVDHPRPARAKVSWTHFQRLGRVVEVPRVE 747
Db 741 CSAINHM-----KKNVEHLPSTFKGMKAIIVDAKPVRAAVTRYHMKELGINVDVTSLK 795
Qy 748 QAL-----HYLKIGT-----TTVMILIEQIWI--NREADDFIKKIQK-----DPLFLSPKL 792
Db 796 TAVVAAAFAFERNGSPLPKQDMLLVKEDSWISTEDNDSIRLNSNTNGNVHHSKSPKL 855
Qy 793 ILLANSVSSISEALCTGIDPPIVIVKPLRASMALATLQRLGIGIREPPQHKGPALIL 852
Db 856 ALFATNITNSEFDRAKSAGFADTVIMKPLRASMIGACIQVLELRKTRQHQHPEGSSPATL 915
Qy 853 RNLLGRKILIVDDNNVLRVAAGALKKYGADVVCASGKAIKAILLPPHFDACFMDIQ 912
Db 916 KSLLTGKILIVDDNINVRRAAGALKKFGAEVVCASGQVAGLGLLQIPHTFDACFMDIQ 975
Qy 913 MPMDGFEATRIRDMEEEMNKRIKNGEALIVENGKTSWHLPLVLTADVIQATHEECL 972
Db 976 MPQMDGFEATRIRMMKEKTEK-----TNLEWHLPLAMTADVIHATYBECL 1023
Qy 973 KCGMDGVSKPFEAEOLYREVSREFN-----SPS 1001
Db 1024 KSGMDGVSKPFEENLYKSAKSKPNPISPS 1056

RESULT 12
US-10-135-322-24
; Sequence 24, Application US/10135322
; Publication No. US20020173017A1
; GENERAL INFORMATION:
; APPLICANT: BENFEY, PN
; APPLICANT: HELARIUTTA, Y
; APPLICANT: MAHONEN, AP
; APPLICANT: BONKE, AWM
; APPLICANT: KAUPPINEN, L
; APPLICANT: RIIKONEN, M
; TITLE OF INVENTION: WOODEN LEG GENE, PROMOTER AND USES THEREOF
; FILE REFERENCE: 5914-086-999
; CURRENT APPLICATION NUMBER: US/10/135,322
; CURRENT FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: 60/253,739
; PRIOR FILING DATE: 2000-11-29
; NUMBER OF SEQ ID NOS: 43
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 24
; LENGTH: 1057
; TYPE: PRT
; ORGANISM: Arabidopsis thaliana
US-10-135-322-24

Query Match 48.0%; Score 2475.5; DB 14; Length 1057;
Best Local Similarity 50.8%; Pred. No. 2.1e-214;
Matches 535; Conservative 156; Mismatches 251; Indels 111; Gaps 18;
Qy 21 MTLTKKKNKMFNKNISSSGLKIPSPS-----YQFLGSYKFN----- 57
Db 43 LNSSEKPRKIDFWR---SGLM--GFAKMQQQQLQHSVAVKMNNNNDLGNKKGSTF 96
Qy 58 ----KAWRKLIVVVVFWVLVSWITWTFWYSSQAMEKREKETLASMCDERARMLQDQPNVS 113
Db 97 IQEHRALLPALILIIIVGFISSGIYQWMDANKIRREEVLYSMCDQARMLQDQPSVS 156
Qy 114 MNHVQAMSLISTPHGKIPSAIDQRTSEYDRTSPERPLTSGVAVAMRVLSEREPE 173
Db 157 VNVHALLIVSIFHYHKNFSAIDQETFAETARTAFERLLSGVAAEKVNFREMF 216

Qy 174 RQOQWTRKMYSLERQNPVHKDDYDEALEPSPVOEYAPVIFAQDTVSHVVSLEMDLSGKE 233
Db 217 RQHNWVTKT-----DRGEPSPVDEYAPVIFSQDSVYLSLESDMWSGEE 261
Qy 234 DRENVLRARSSGKGLTAPPLIKTNELGVLITFAVVKRDLPSNATPKERIEATNGVLGG 293
Db 262 DRENILKARETGKAVLTPPRLLETHLGVVLTFFPVYKSSLPENPTVEERIAATAGVLGG 321
Qy 294 VFDESIVENLLOQLASKQITLVNVDITNHSQIPSMYGT-NVSAD-GLERSVSLIFGDP 351
Db 322 AFDVESIVENLLOQLAGNQALVHVVDITNADSLVWYGNQDEADRSLSHESKLDGDP 381
Qy 352 LRKHEMCRKQKQPPVPLSNVTSFGILVIALVAHIHATVSRHKEVEDCDKMKQK 411
Db 382 FRKHMI CRYHQKAPIPLNVLTTPVLPFAIGFLVGYILYGAAMHIKVVEDDFHEMQLKV 441
Qy 412 KAAEADVAKSQFATVSHETRTPMNGVGLMMLMOTELDVTQODYVTRTAQASKALVSL 471
Db 442 RAAEADVAKSQFATVSHETRTPMNGILGLMLLDTLSSTORDYATQACVCGKALIAL 501
Qy 472 INEVLDAKIESGKLEEEVRFDLRGILDDVLSLFSKSOQKGVELAVYISDRVPMGLIG 531
Db 502 INEVLDAKIEAGKLELESVFFDIRSLDDVLSLFSSESRNKSIELAVFVSDKVPEIVKG 561
Qy 532 DPGFRQILNLMGNSIKFTTEKGHIFVTVHLVDLSEIDGETA-----SS 577
Db 562 DSGRFRQIILNLVNSVKFTTEKGHIFVKVHLAEQSKDESEPKNALNGVSEEMIVSKQS 621
Qy 578 PESTLSGLPVADRQRSHENKAFSSNGH--RSPEPSPDINLIVSVEDTGVGIVPEAQSR 635
Db 622 SYNTLSGYEADGRNSWDFKHLVSEESQSLSEFDS-SNRLMWSIEDTGIGIPLVAQGR 680
Qy 636 IFTPMQVGPISRTHTGGTIGLSISKCLVGLMKGEIGFSSTPKVGSFTFTAVFS---- 691
Db 681 VFMPFQADSSSTRNYGGTIGLSISKCLVGLMRGQINFISRPHIGSTFTFTAVLEKCDK 740
Qy 692 ---NGMQPAERKNDNQPISEFRCMKAVVDHPRPARAKVSWTHFQRLGRVVEVPRVE 747
Db 741 CSAINHM-----KKNVEHLPSTFKGMKAIIVDAKPVRAAVTRYHMKELGINVDVTSLK 795
Qy 748 QAL-----HYLKIGT-----TTVMILIEQIWI--NREADDFIKKIQK-----DPLFLSPKL 792
Db 796 TAVVAAAFAFERNGSPLPKQDMLLVKEDSWISTEDNDSIRLNSNTNGNVHHSKSPKL 855
Qy 793 ILLANSVSSISEALCTGIDPPIVIVKPLRASMALATLQRLGIGIREPPQHKGPALIL 852
Db 856 ALFATNITNSEFDRAKSAGFADTVIMKPLRASMIGACIQVLELRKTRQHQHPEGSSPATL 915
Qy 853 RNLLGRKILIVDDNNVLRVAAGALKKYGADVVCASGKAIKAILLPPHFDACFMDIQ 912
Db 916 KSLLTGKILIVDDNINVRRAAGALKKFGAEVVCASGQVAGLGLLQIPHTFDACFMDIQ 975
Qy 913 MPMDGFEATRIRDMEEEMNKRIKNGEALIVENGKTSWHLPLVLTADVIQATHEECL 972
Db 976 MPQMDGFEATRIRMMKEKTEK-----TNLEWHLPLAMTADVIHATYBECL 1023
Qy 973 KCGMDGVSKPFEAEOLYREVSREFN-----SPS 1001
Db 1024 KSGMDGVSKPFEENLYKSAKSKPNPISPS 1056

RESULT 13
US-10-126-120-2
; Sequence 2, Application US/10126120
; Publication No. US20030108526A1
; GENERAL INFORMATION:
; APPLICANT: Sakakibara, Hitoshi
; APPLICANT: Takei, Kenlaro
; TITLE OF INVENTION: MICROORGANISMS FOR USE IN THE MEASUREMENT OF ENVIRONMENTAL FACTS
; FILE REFERENCE: 11127-004001
; CURRENT APPLICATION NUMBER: US/10/126,120
; CURRENT FILING DATE: 2002-04-19
; PRIOR APPLICATION NUMBER: JP 2001-291059

; PRIOR FILING DATE: 2001-09-25
; NUMBER OF SEQ ID NOS: 50
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 2
; LENGTH: 974
; TYPE: PRT
; ORGANISM: Zea mays
US-10-126-120-2

Query Match 47.7%; Score 2462; DB 15; Length 974;
Best Local Similarity 51.8%; Pred. No. 3e-213;
Matches 512; Conservative 161; Mismatches 246; Indels 70; Gaps 14;

QY 58 KAWMKLVVV-WVFWVLVSIWTFWFSSQAMEKKEKTLASCDERARMLOQFVNMVH 116
Db 11 KKWMEGLAAGVLTAVVCSAVNHHVTLRSDRAERLVNCEERARMLOQFGVTNVH 70

QY 117 VOAMSLISTFHGKIPSAIDORTSEYTDRTSFERPLTSGVAYAMRVLHSHREFFERQO 176
Db 71 VHAIALISTFNFESPPAIDQDTAKYTARTISFERPLNGVAFQRFVHHEREFESQO 130

QY 177 GWTIRKMSLEQNPVHKDDYDLEALEPSPVQBEYAPVIPAQDTVSHVSLDMLSGKEORE 236
Db 131 GWMVNTMQR-----EPAPQVEYAPVIFSQDTVSLARIDMWSGEEDRE 174

QY 237 NVLRARSSGKGVLTAPPFLIKTNRLGVILTFVAYKEDLPSTNATPKERTBATNGYLGVPD 296
Db 175 NIFRARTTGKAVITNPFRLGNSHGLVLTFAVYRDLFPADASVQRVEATTGYLGAPD 234

QY 297 IESLVENLLQQALSKQTLVNVYDITNHSQPSMYGTNVSDGLE--RVSPILFGDPLRK 354
Db 235 VESLVENLLSKLAGNQDIVNVYDVTNADAMVLGPSSLDQVFLVSLMDLFGDPRK 294

QY 355 HEMRCRFKQKPPWVLSMTVSFGLIVALLVAHIHATVSRIRHKVEEDCDNMKQLKXAE 414
Db 295 HEMRCRYRQKLPWPSAITNPLGTFTVIMLLGYSTAAAYSRVYDKVTEDCRKMEELKQAE 354

QY 415 ADVAKSQFLATVSHIETPMNGVLGMLHMLMDTDLVTOQDYVRTAQASGKALVSLINE 474
Db 355 AADVAKSQFLATVSHIETPMNGVLGMLDMLGTDLTMTQKDYAQTAQMCGRALITLND 414

QY 475 VLDQAKIESGKLEBEVRDLRGLDLDVLSFSSKQKGVELAVVSDRPVDMILGPG 534
Db 415 VLDRAKIAGKLEAEVAPDLRLMDDDVVLSFSKREKICELAEVFCNVPKVPGLDPW 474

QY 535 RFRQILTNLGMNSIKPTEKHIFVTVHLVDE-----LPESIDGE-----TASSPES 580
Db 475 RFRQILTNLGVNAVKFTEGHVFRVCLAEANSMEANQVLHGAMNGKGRVESTANGAFN 534

QY 581 TLSGLPVDROBSWENKFAFSN-----CHRSFSPSPDINLIVSDEVTGVIPE 631
Db 535 TUSGFEADRNSWQYFKLLSDKESLDDLESENQSDSDRVTLAISIEDTGVGIPQ 594

QY 632 AQSRIFTPMQVGPSTSRTHGCTGIGLSISKVLGMLKGEIGFSSTPKVGSFTFTTAVFS 691
Db 595 AQDRVFTPMQADSTSRNYGCTGIGLSISKLAELMGQIISFTSHPSVGSFTFTSATLK 654

QY 692 NGMQ--PAERKNDNNQPISEFRGMKAVVDRHRPAKAVSWYHFORLGRVVEVPRVQA 749
Db 655 HSHKDISGDSRSSLTALPTAFKGMKAILVDCRPVRSVATRVHLKRLGILLQVNNMNAV 714

QY 750 LHYL-----KIGT-TTVNMLILEQELWNREAD-----DFIKLKQDPLFLSPKLIILANSV 799
Db 715 VKAFPGQNGAAGRSKASILFIESDFPWRPETDVQLNLHLEQNGQLSGDHKRWLLVTSB 774

QY 800 E-----SSISEALCTGIDPPIVIVPLRASMLAATLQRGIGIGIREPPQHGPPALIRN 854
Db 775 ADKDKYGSIFD-----IWCXPIRASTASSIIQQLLKVEIAERKDNQNRPS-FLRS 824

QY 855 LLLGKILIVDDNNVNLRAAGALKKYGADVVCABSIGKAIKSLKKPHEFDACFNQDIQMP 914
Db 825 LLVGNILVDDNKVNLRAVAAALKKYGANVCSVSGDKDAISLLQPPHFRFDACFNQVMP 884

QY 915 EMDGFEATRRIRDMEEENKRIKNGEALIVENGKTSWHLPLVLAANTADVIQATHEBCKC 974
Db 885 EMDGFEATGQIRQWELKANEERKNKLASI-EGSTTAHYHLPLVLAANTADVIQATVEBCKS 943

QY 975 GMDGVSKPPEAEQOLYREVSRFFNSPST 1003
Db 944 GMDGVSKPPEDEEQLYQAVSRLVVGTTDS 972

RESULT 14
US-10-101-464A-978
; Sequence 978, Application US/10101464A
; Publication No. US20030046728A1
; GENERAL INFORMATION:
; APPLICANT: Strabala, Timothy
; APPLICANT: Nieuwenhuizen, Nicolaas
; APPLICANT: Higgins, Colleen M.
; TITLE OF INVENTION: Compositions Isolated from Plant Cells
; FILE REFERENCE: 11000.1020C2
; CURRENT APPLICATION NUMBER: US/10101.464A
; PRIOR FILING DATE: 2002-03-18
; PRIOR APPLICATION NUMBER: 09/704,302
; PRIOR FILING DATE: 2000-11-01
; PRIOR APPLICATION NUMBER: 09/228,986
; PRIOR FILING DATE: 1999-01-12
; PRIOR APPLICATION NUMBER: 60/162,866
; PRIOR FILING DATE: 1999-11-01
; PRIOR APPLICATION NUMBER: PCT/US00/00724
; NUMBER OF SEQ ID NOS: 989
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 978
; LENGTH: 480
; TYPE: PRT
; ORGANISM: Eucalyptus grandis
US-10-101-464A-978

Query Match 26.5%; Score 1368.5; DB 15; Length 480;
Best Local Similarity 59.2%; Pred. No. 9.3e-115;
Matches 277; Conservative 72; Mismatches 98; Indels 21; Gaps 3;

QY 48 YQFLGSKFKENKAWRKLVVVWVFWVLVSIWTFWFSSQAMEKKEKTLASCDERARMLO 107
Db 26 YTFIQS---NRATPKILVLVSWGVKAFLSMIYRKMDADIKVRREKEVLVSCDQFARMLK 82

QY 108 DQFNVMNHVQAMSLISTFHGKIPSAIDORTSEYTDRTSFERPLTSGVAYAMRVLHS 167
Db 83 DQFSVSNHVALAILVSTFHYKNPSPALDQETTAETARTAFERPLLSGVAYAEVTVNS 142

QY 168 BREFERQOGWTIRKMSLEQNPVHKDDYDLEALEPSPVQBEYAPVIPAQDTVSHVSLD 227
Db 143 BREKPEEQHGWTKITMEK-----QSPVRDEYAPVIFSQETVSYESLD 186

QY 228 MLSGKEORENVLRARSSGKGVLTAPPFLIKTNRLGVILTFVAYKEDLPSTNATPKERTBAT 287
Db 187 MWSGEORENLTIRARATGKAVLTSFRLGSHGLVLTFFVYKSKLPNPNFTVEERTEAT 246

QY 288 NGYLGGVDFDIESLVENLLQQALSKQTLVNVYDITNHSQPSMYGTNVSA--DGLERVSP 345
Db 247 VGYLGGAFDVESLVENLLQDLGNQAILVNVYDVTNSEPLIMYGHQVQECDDTSLHESK 306

QY 346 LIPGDDPLRKHEMRCRFKQKPPWVLSMTVSFGLIVALLVAHIHATVSRIRHKVEEDCDK 405
Db 307 LDGDPFRKHQMIKRYHQKAPPSWTALTATFAFFVGLLVGYLYGAATHIVKVEDDFHE 366

QY 406 MKQLKKAARADVAKSQFLATVSHIETPMNGVLGMLHMLMDTDLVTOQDYVRTAQASG 465
Db 367 MQELKVRAEAADVAKSQFLATVSHIETPMNGILGMLALLDTELSTQDYAQTAQICG 426

QY 466 KALVSLINEVLDQAKIESGKLEBEVRDLRGLDLDVLSFSSKQK 513
Db 427 KALIALINEVLDRAKIEAGKLELETVTFDINSILDDVLSLFSSESRHK 474

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: November 28, 2003, 13:58:54 ; Search time 35.4302 Seconds
(without alignments)
7698.569 Million cell updates/sec

Title: US-09-918-508-6
Perfect score: 5397
Sequence: 1 MNWLNHHQEEBEPRIE.....ENLYKSVAKSKFNPIPS 1057

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 830525 seqs, 258052604 residues

Total number of hits satisfying chosen parameters: 830525

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SPTRMBL 23.3

- 1: sp_archea.*
- 2: sp_bacteria.*
- 3: sp_fungi.*
- 4: sp_human.*
- 5: sp_invertebrate.*
- 6: sp_mammal.*
- 7: sp_mhc.*
- 8: sp_organelle.*
- 9: sp_phage.*
- 10: sp_plant.*
- 11: sp_rodent.*
- 12: sp_virus.*
- 13: sp_vertebrate.*
- 14: sp_unclassified.*
- 15: sp_rvirus.*
- 16: sp_bacteriap.*
- 17: sp_archaeap.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	5397	100.0	1057	10 Q9C5T9	Q9C5T9 arabidopsis
2	5397	100.0	1080	10 Q9C5T8	Q9C5T8 arabidopsis
3	5387	99.8	1057	10 Q9S1T0	Q9S1T0 arabidopsis
4	5387	99.8	1080	10 Q9C5U0	Q9C5U0 arabidopsis
5	2705.5	50.1	974	10 Q9FRY7	Q9FRY7 zea mays (m
6	2546	47.2	1176	10 Q9CSU2	Q9CSU2 arabidopsis
7	2534.5	47.0	1173	10 Q9FKH3	Q9FKH3 arabidopsis
8	2485	46.0	1036	10 Q9CSU1	Q9CSU1 arabidopsis
9	2431.5	45.1	1041	10 Q8L8I6	Q8L8I6 catharanthu
10	2402	44.5	1092	10 Q9FZK3	Q9FZK3 arabidopsis
11	2375	44.0	1023	10 Q8RYG4	Q8RYG4 oryza sativ
12	2248.5	41.7	925	10 Q8S6P5	Q8S6P5 oryza sativ
13	1698.5	31.5	652	10 Q8GUG0	Q8GUG0 arabidopsis
14	1042	19.3	627	10 Q9AUO0	Q9AUO0 oryza sativ
15	806.5	14.9	1765	16 Q8E1I0	Q8E1I0 shewanella
16	792.5	14.7	1268	2 Q8KQV0	Q8KQV0 vibrio chol

ALIGNMENTS

RESULT 1

Q9C5T9 ID Q9C5T9 PRELIMINARY; PRT; 1057 AA.

AC Q9C5T9; 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Cytokinin receptor CRE1a.

GN CRE1.

OS Arabidopsis thaliana (Mouse-ear cress).

OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;

OC eurosids II; Brassicales; Brassicaceae; Arabidopsi

OX NCBI_TaxID=3702;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN=cv. Wassilewskija;

RA Inoue T., Higuchi M., Hashimoto Y., Seki M., Kobayashi M., Kato T.,

RA Satoishi T., Shinoraki K., Kakimoto T.;

RT "Identification of a cytokinin receptor, CRE1, from Arabidopsis.";

RL Submitted (OCT-2000) to the EMBL/GenBank/DBJ databases.

DR EMBL; AB049934; BAB3310.1; -

DR HSSP; P06657; 2CHF.

DR InterPro; IPR001594; ATPbind_ATPase.

DR InterPro; IPR006189; CHASE

DR InterPro; IPR003661; His_kinA.

DR InterPro; IPR005467; His_kinase.

DR InterPro; IPR001789; Response_reg.

DR Pfam; PF03924; CHASE; 1.

DR Pfam; PF02518; HATPase_c; 1.

DR Pfam; PF00512; HSKA; 1.

DR Pfam; PF00072; response_reg; 1.

DR ProDom; PD000039; Response_reg; 1.

DR SMART; SM00387; HATPase_c; 1.

DR SMART; SM00388; HSKA; 1.

DR SMART; SM00448; RSC; 1.

DR PROSITE; PS50839; CHASE; 1.

DR PROSITE; PS50109; HIS_KIN; 1.

DR PROSITE; PS50110; RESPONSE_REGULATORY; 1.

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Q8PJN8 xanthomonas
P73035 synechocyst
Q9HWR8 pseudomonas
Q8YQG8 anabaena sp
Q8DJE3 synechococc
Q95PH6 dictyosteli
Q8D68 vibrio vuln
Q8P883 xanthomonas
Q8YUQ6 anabaena sp
Q8DI3 synechococc
Q9KSB0 vibrio chol
Q8D5E0 vibrio vuln
Q8Z445 salmonella
Q919E4 salmonella
Q8EJ91 shewanella
Q8YF51 anabaena sp
Q32556 pectobacter
Q98FG5 rhizobium l
Q8GMB7 pantoaea agg
Q9KPC0 vibrio chol
Q31138 pseudomonas
Q23853 dictyosteli
Q08235 pectobacter
Q88F11 rhizobium l
Q8HYE4 pseudomonas
Q8RMF4 acinetobact
Q9ZNG1 pseudomonas
Q8EKG2 shewanella

17 790.5 14.6 1261 16 P73926
18 785 14.5 1364 16 Q8PJN8
19 777 14.4 1462 16 P73035
20 772.5 14.3 1417 16 Q9HWR8
21 771.5 14.3 1550 16 Q8YQG8
22 767.5 14.2 1353 16 Q8DJE3
23 764.5 14.2 2082 5 Q95PH6
24 757 14.0 928 16 Q8D68
25 752.5 13.9 1364 16 Q8P883
26 750.5 13.9 1299 16 Q8YUQ6
27 740 13.7 1035 16 Q8DI3
28 729.5 13.5 1331 16 Q9KSB0
29 726.5 13.5 1320 16 Q8D5E0
30 725 13.5 918 16 Q8Z445
31 725 13.4 918 16 Q919E4
32 725 13.4 1188 16 Q8EJ91
33 721 13.4 1817 16 Q8YF51
34 717 13.3 928 2 Q32556
35 715.5 13.3 786 16 Q98FG5
36 708.5 13.1 908 2 Q8GMB7
37 707 13.1 927 16 Q9KPC0
38 704 13.0 925 16 Q31138
39 702 13.0 2150 5 Q23853
40 695.5 12.9 929 2 Q08235
41 695.5 12.9 1391 16 Q88F11
42 693.5 12.8 919 16 Q8HYE4
43 692.5 12.8 935 2 Q8RMF4
44 685 12.7 917 2 Q9ZNG1
45 685 12.7 929 16 Q8EKG2


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Db 264 VIFSQDSVSYLESIDMSGSEEDRENILRARETGKAVLTSPRLLETHHLGVVLPFPVYKS 323
Qy 301 SLPENPTVEERIAATAGVLGAFDVESLVENLLQOLAGNOAIVVHVYDITNASDPLVMYG 360
Db 324 SLPENPTVEERIAATAGVLGAFDVESLVENLLQOLAGNOAIVVHVYDITNASDPLVMYG 383
Qy 361 NQDEEADRSLSHESKLDGDFPRKHMI CRVHQKAPIPLNVLTTVPLFAIGLVGYLY 420
Db 384 NQDEEADRSLSHESKLDGDFPRKHMI CRVHQKAPIPLNVLTTVPLFAIGLVGYLY 443
Qy 421 GAAMHIVKVEDDFHEMQELKVRAEADVAKSQFLATVSHERTPMNGILGMLMLDTEL 480
Db 444 GAAMHIVKVEDDFHEMQELKVRAEADVAKSQFLATVSHERTPMNGILGMLMLDTEL 503
Qy 481 SSTORDYAQTAVCGKALIALINEVLDRAKTEAGKLELESVFPDIRSLDVLSPSEES 540
Db 504 SSTORDYAQTAVCGKALIALINEVLDRAKTEAGKLELESVFPDIRSLDVLSPSEES 563
Qy 541 RNKGIELAVFVSDKVPETVKGDSGRFQIIINLVGNSVKFTEKGHIFVKVHLAQSKDES 600
Db 564 RNKGIELAVFVSDKVPETVKGDSGRFQIIINLVGNSVKFTEKGHIFVKVHLAQSKDES 623
Qy 601 EPKQNALGVSEEMIVVSKQSYNTLSGYEAADGRNSWDSFKHLVSEQSLSEFDISSNV 660
Db 624 EPKQNALGVSEEMIVVSKQSYNTLSGYEAADGRNSWDSFKHLVSEQSLSEFDISSNV 683
Qy 661 RLMVSIEDTGIGIPLVAGRVFMPFMOADSTSRNYGGTGIGLSISKCLVELMRGQINFI 720
Db 684 RLMVSIEDTGIGIPLVAGRVFMPFMOADSTSRNYGGTGIGLSISKCLVELMRGQINFI 743
Qy 721 SRPHIGSTFWTAVLEKDKCSAINHMKKPNVHLPTSTFKGKAIIVDAKVPRAAVTRYH 780
Db 744 SRPHIGSTFWTAVLEKDKCSAINHMKKPNVHLPTSTFKGKAIIVDAKVPRAAVTRYH 803
Qy 781 MKRLGINVDVTSLSKTA VAAAFERNGPSLPKTPQLDMILVEKDSWISTEDNSEIRLL 840
Db 804 MKRLGINVDVTSLSKTA VAAAFERNGPSLPKTPQLDMILVEKDSWISTEDNSEIRLL 863
Qy 841 NSRNGNVHHSKPKALPATNITSEFDRKASGADFTVIMKPLRASMIGACLOQVLELR 900
Db 864 NSRNGNVHHSKPKALPATNITSEFDRKASGADFTVIMKPLRASMIGACLOQVLELR 923
Qy 901 KTRQHPGSSPATILKSLITGKILVDDNTVNRVAAAGALKKFGAEVVCAGSQVALGL 960
Db 924 KTRQHPGSSPATILKSLITGKILVDDNTVNRVAAAGALKKFGAEVVCAGSQVALGL 983
Qy 961 LQIHPTFDACFMDIQMPQMDGFEATQIRMMKEAKEKTNLEWHLPILAMTADVIHATYE 1020
Db 984 LQIHPTFDACFMDIQMPQMDGFEATQIRMMKEAKEKTNLEWHLPILAMTADVIHATYE 1043
Qy 1021 ECLKSGMDGYVSKPFEENLYKSAKSPKPNPISPS 1057
Db 1044 ECLKSGMDGYVSKPFEENLYKSAKSPKPNPISPS 1080

RESULT 3
Q9SITO PRELIMINARY; PRT; 1057 AA.
ID AC Q9SITO; Q9FD23;
AC Q9SITO; Q9FD23;
DT 01-MAY-2000 (TremBLrel. 13, Created)
DT 01-JUN-2002 (TremBLrel. 21, Last sequence update)
DT 01-MAR-2003 (TremBLrel. 23, Last annotation update)
DE Putative histidine kinase (Putative histidine kinase receptor).
GN AT2G01830 OR WOL.
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eurosids II; Brassicales; Brassicaceae; Arabidopsis.
OX NCBI_TaxID=3702;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=cv. Columbia;
RA Lin X., Kaul S., Shea T.P., Fujii C.Y., Shen M., VanAken S.B.,
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RA Barnstead M.E., Mason T.M., Bowman C.L., Ronning C.M., Benito M.-I.,
RA Carrera A.J., Creasy T.H., Buell C.R., Town C.D., Nierman W.C.,
RA Fraser C.M., Venter J.C.;
RL Submitted (FEB-2002) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Root;
RX PubMed=11114883;
RA Mahonen A., Bonke M.A., Kauppinen L., Riikonen M., Benfey P.N.,
RA Helariutta Y.;
RT A novel two-component hybrid molecule regulates the vascular pattern
of the Arabidopsis root.;
RL Genes Dev. 14:2938-2943(2000).
DR EMBL; AC007069; AAD21777.2; -
DR EMBL; AJ278530; CAC18523.1; -
DR EMBL; AJ278528; CAC18521.1; -
DR EMBL; AJ278529; CAC18522.1; -
DR HSSP; P06143; ID4Z
DR InterPro; IPR003594; ATPbind_ATPase.
DR InterPro; IPR004358; Bact_sens_pr_C.
DR InterPro; IPR006189; CHASE.
DR InterPro; IPR003661; His_kinA.
DR InterPro; IPR005467; His_kinase.
DR InterPro; IPR001789; Response_reg.
DR Pfam; PF03924; CHASE; 1.
DR Pfam; PF02518; HATPase_c; 1.
DR Pfam; PF00512; Hiska; 1.
DR Pfam; PF00072; response_reg; 1.
DR PRINTS; PR00344; BCTRLSENSOR.
DR ProDom; PD000039; Response_reg; 1.
DR SMART; SM00387; HATPase_c; 1.
DR SMART; SM00388; Hiska; 1.
DR SMART; SM00448; REC; 1.
DR PROSITE; PS50839; CHASE; 1.
DR PROSITE; PS50109; HIS_KIN; 1.
DR PROSITE; PS50110; RESPONSE_REGULATORY; 1.
KW Kinase; Phosphorylation; Receptor; Sensory transduction.
SQ SEQUENCE 1057 AA; 117954 MW; E1381C8685F0D787 CRC64;

Query Match 99.8%; Score 5387; DB 10; Length 1057;
Best Local Similarity 99.8%; Pred. No. 0;
Matches 1055; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 MNWALNNHQEBEPRRIEISDESLENLKSDFYQLGGGALNSSEKPKRIDFWRSGLM 60
Db 1 MNWALNNHQEBEPRRIEISDESLENLKSDFYQLGGGALNSSEKPKRIDFWRSGLM 60
Qy 61 GFAMQOQOQLOHSVAVKMNNNNDLMGNKKGSTFTQEHRLALPKALILWIIIVGRISS 120
Db 61 GFAMQOQOQLOHSVAVKMNNNNDLMGNKKGSTFTQEHRLALPKALILWIIIVGRISS 120
Qy 121 GIYQWMDANKIRREEVLSWCDORARMLOQOFSVSNVHVHALAILYSTFHYHKNPSAID 180
Db 121 GIYQWMDANKIRREEVLSWCDORARMLOQOFSVSNVHVHALAILYSTFHYHKNPSAID 180
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Db 181 QETFAEYTAFTAFERPLLSGVAYAEKVNFNERFERQHNNVKTMDRGPSVPVRDEYAP 240
Qy 241 VIFSQDSVSYLESIDMSGSEEDRENILRARETGKAVLTSPRLLETHHLGVVLPFPVYKS 300
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Qy 361 NQDEEADRSLSHESKLDGDFPRKHMI CRVHQKAPIPLNVLTTVPLFAIGLVGYLY 420
Db 361 NQDEEADRSLSHESKLDGDFPRKHMI CRVHQKAPIPLNVLTTVPLFAIGLVGYLY 420
Qy 421 GAAMHIVKVEDDFHEMQELKVRAEADVAKSQFLATVSHERTPMNGILGMLMLDTEL 480
Db 421 GAAMHIVKVEDDFHEMQELKVRAEADVAKSQFLATVSHERTPMNGILGMLMLDTEL 480
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Db 421 GAAMHIVKVEDDFHEMQLKVRBAADVAKSOFATVSHSHEIRTPMNGILGMLAMDTEL 480
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Db 481 SSTQDYAQTACVCGKALIALINEVLDRAKIEAGKLELESVPDIRSILDDVLSLFSSES 540
QY 541 RNKGIELAVFVSDKVEIIVKGDGRFROIINLVGNSVFKTEKHIFVKVHLAEQSKDES 600
Db 541 RNKSIELAVFVSDKVEIIVKGDGRFROIINLVGNSVFKTEKHIFVKVHLAEQSKDES 600
QY 601 EPKNALGVSEEMIVVSKOSSNTLSGYEADGRNSWDSFKHLVSEFQSLSEFIDSSNV 660
Db 601 EPKNALGVSEEMIVVSKOSSNTLSGYEADGRNSWDSFKHLVSEFQSLSEFIDSSNV 660
QY 661 RLWVSIEDTGIGIPLVAQGRVPMFQADSSSTRNYGGTGIGLSISKCLVELMRGQINFI 720
Db 661 RLWVSIEDTGIGIPLVAQGRVPMFQADSSSTRNYGGTGIGLSISKCLVELMRGQINFI 720
QY 721 SRPHIGSTFWTAVLEKCDKCSAINHMKPNVHEHLPSTFKGMKAIIVDAKPVRAAVTRYH 780
Db 721 SRPHIGSTFWTAVLEKCDKCSAINHMKPNVHEHLPSTFKGMKAIIVDAKPVRAAVTRYH 780
QY 781 MKRLGINVDVVTSLKTAIVAAAFERNGLPTKPOLDMILVEKDSWISTEDNDSIRLL 840
Db 781 MKRLGINVDVVTSLKTAIVAAAFERNGLPTKPOLDMILVEKDSWISTEDNDSIRLL 840
QY 841 NSRTNGNVHKSFKPLALFATNITNSFDRAKSAGFADTVIMKPLRASMIGACILQOVLELR 900
Db 841 NSRTNGNVHKSFKPLALFATNITNSFDRAKSAGFADTVIMKPLRASMIGACILQOVLELR 900
QY 901 KTRQHPGESSPATLKSLLTGKILVDDNIIVNRVAAGALKKFGAEVVCASGGQVALGL 960
Db 901 KTRQHPGESSPATLKSLLTGKILVDDNIIVNRVAAGALKKFGAEVVCASGGQVALGL 960
QY 961 LOIPHTFDACFMDIQMPDQGFATQIRNMEKEAKEKTNLEWHLPIILAMTADVIHATYE 1020
Db 961 LOIPHTFDACFMDIQMPDQGFATQIRNMEKEAKEKTNLEWHLPIILAMTADVIHATYE 1020
QY 1021 ECLKSGMDGVSKPFEENLYKSVAKSFKPNPISPSS 1057
Db 1021 ECLKSGMDGVSKPFEENLYKSVAKSFKPNPISPSS 1057

RESULT 4
Q9CSU0 PRELIMINARY; PRT; 1080 AA.
AC Q9CSU0;
DT 01-JUN-2001 (TrEMBLrel 17, Created)
DT 01-JUN-2001 (TrEMBLrel 17, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel 23, Last annotation update)
DE Histidine kinase.
GN AHK4.
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eurosids II; Brassicales; Brassicaceae; Arabidopsi.
OX NCBI_TaxID=3702;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21154803; PubMed=11230578;
RA Ueguchi C.; Koizumi H.; Suzuki T.; Mizuno T.;
RT "Novel family of sensor histidine kinase genes in Arabidopsis
thaliana.";
RL Plant Cell Physiol. 42:231-235(2001).
DR EMBL; AB046871; BAB40776.1; -.
DR HSSP; P06657; 2CHF.
DR InterPro; IPR003594; ATPbind_ATPase.
DR InterPro; IPR006189; CHASE.
DR InterPro; IPR003661; His_kinase.
DR InterPro; IPR005467; His_kinase.
DR InterPro; IPR001789; Response_reg.
DR Pfam; PF03924; CHASE; 1.
DR Pfam; PF02518; HATPase_C; 1.

DR Pfam; PF00512; Hiska; 1.
DR Pfam; PF00072; response_reg; 1.
DR ProDom; PD000039; Response_reg; 1.
DR SMART; SM00387; HATPase_c; 1.
DR SMART; SM00388; Hiska; 1.
DR SMART; SM00448; REC; 1.
DR PROSITE; PS50839; CHASE; 1.
DR PROSITE; PS50109; HIS_KIN; 1.
DR PROSITE; PS50110; RESPONSE_REGULATORY; 1.
KW Kinase; Phosphorylation; Sensory transduction.
SQ SEQUENCE 1080 aa; 120730 MW; 5950DB968B529401 CRC64;

Query Match 99.8%; Score 5387; DB 10; Length 1080;
Best Local Similarity 99.8%; Pred. No. 0;
Matches 1055; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 MNWLNHNQEEEEPRRIEISDSSELENLKSDFYQLGGGALNSESSEPKRDKIDFRSGLM 60
Db 24 MNWLNHNQEEEEPRRIEISDSSELENLKSDFYQLGGGALNSESSEPKRDKIDFRSGLM 83
QY 61 GFAPKMQQQQLQHSVAVFMNNNNNDLMGNKKGSTFIQEHRAALLPKALILWIIIVGFISS 120
Db 84 GFAPKMQQQQLQHSVAVFMNNNNNDLMGNKKGSTFIQEHRAALLPKALILWIIIVGFISS 143
QY 121 GIYQWMDANKTRRBEVLVSMCDQARMLOQFQSVSVNVHVALAILVSTFHHKMPASID 180
Db 144 GIYQWMDANKTRRBEVLVSMCDQARMLOQFQSVSVNVHVALAILVSTFHHKMPASID 203
QY 181 QSTFAEYRTAFARPLLSGVAYAEKVNFEREEMERQHNWIKTMDRGEPSVDEYAP 240
Db 204 QSTFAEYRTAFARPLLSGVAYAEKVNFEREEMERQHNWIKTMDRGEPSVDEYAP 263
QY 241 VIFSQDSVSYLESLOMMSGEEDRENILRARETGKAVLTSPPFRLLETHLGVVLTFFPVYKS 300
Db 264 VIFSQDSVSYLESLOMMSGEEDRENILRARETGKAVLTSPPFRLLETHLGVVLTFFPVYKS 323
QY 301 SLUPNPTVEERTAAATAGLGGAFVSEVLNLLQOLAGNQAIIVHVYDITNASDPLVMYG 360
Db 324 SLUPNPTVEERTAAATAGLGGAFVSEVLNLLQOLAGNQAIIVHVYDITNASDPLVMYG 383
QY 361 NODEEADRSLSHESKLDGDPFRHKMICRVHQKAPIPLNVLTTVPLFATGFLVGYILY 420
Db 384 NODEEADRSLSHESKLDGDPFRHKMICRVHQKAPIPLNVLTTVPLFATGFLVGYILY 443
QY 421 GAAMHIVKVEDDFHEMQLKVRBAADVAKSOFATVSHSHEIRTPMNGILGMLAMDTEL 480
Db 444 GAAMHIVKVEDDFHEMQLKVRBAADVAKSOFATVSHSHEIRTPMNGILGMLAMDTEL 503
QY 481 SSTQDYAQTACVCGKALIALINEVLDRAKIEAGKLELESVPDIRSILDDVLSLFSSES 540
Db 504 SSTQDYAQTACVCGKALIALINEVLDRAKIEAGKLELESVPDIRSILDDVLSLFSSES 563
QY 541 RNKGIELAVFVSDKVEIIVKGDGRFROIINLVGNSVFKTEKHIFVKVHLAEQSKDES 600
Db 564 RNKSIELAVFVSDKVEIIVKGDGRFROIINLVGNSVFKTEKHIFVKVHLAEQSKDES 623
QY 601 EPKNALGVSEEMIVVSKOSSNTLSGYEADGRNSWDSFKHLVSEFQSLSEFIDSSNV 660
Db 624 EPKNALGVSEEMIVVSKOSSNTLSGYEADGRNSWDSFKHLVSEFQSLSEFIDSSNV 683
QY 661 RLWVSIEDTGIGIPLVAQGRVPMFQADSSSTRNYGGTGIGLSISKCLVELMRGQINFI 720
Db 684 RLWVSIEDTGIGIPLVAQGRVPMFQADSSSTRNYGGTGIGLSISKCLVELMRGQINFI 743
QY 721 SRPHIGSTFWTAVLEKCDKCSAINHMKPNVHEHLPSTFKGMKAIIVDAKPVRAAVTRYH 780
Db 744 SRPHIGSTFWTAVLEKCDKCSAINHMKPNVHEHLPSTFKGMKAIIVDAKPVRAAVTRYH 803
QY 781 MKRLGINVDVVTSLKTAIVAAAFERNGLPTKPOLDMILVEKDSWISTEDNDSIRLL 840
Db 804 MKRLGINVDVVTSLKTAIVAAAFERNGLPTKPOLDMILVEKDSWISTEDNDSIRLL 863
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Qy 901 KTRQHPGSSPATLKSLLTGKILVDDNIVNRRVAAGALKKFGAEVVCASGQVALGL 960
Db 924 KTRQHPGSSPATLKSLLTGKILVDDNIVNRRVAAGALKKFGAEVVCASGQVALGL 983
Qy 961 LOIHPHTFACPMQDQFQATQIRMEKEAETNLEWHLPIILAMTADVIHATYE 1020
Db 984 LOIHPHTFACPMQDQFQATQIRMEKEAETNLEWHLPIILAMTADVIHATYE 1043
Qy 1021 ECLSGMDGYVSKPPEENLYKSAKSPKPNIPSPSS 1057
Db 1044 ECLSGMDGYVSKPPEENLYKSAKSPKPNIPSPSS 1080

RESULT 5
Q9FRV7
ID Q9FRY7 PRELIMINARY; PRT; 974 AA.
AC Q9FRY7;
DT 01-MAR-2001 (TremBLrel. 16, Created)
DT 01-MAR-2001 (TremBLrel. 16, Last sequence update)
DT 01-MAR-2003 (TremBLrel. 23, Last annotation update)
DE Histidine kinase 1.
GN ZMHK1
OS Zea mays (Maize).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC PACAD clade; Panicoideae; Andropogoneae; Zea.
OX NCBI_TaxID=4577;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=cv. Golden Cross Bantam T51;
RA Sakakibara H., Sugiyama T.;
RT "Cloning and characterization of maize response regulators.";
RL Submitted (APR-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AB042270; BAB20583.1; -.
DR HSRP; P06143; IAB6.
DR InterPro; IPR003594; ATPbind_ATPase.
DR InterPro; IPR004358; Bact_sens_pr_C.
DR InterPro; IPR006189; CHASE.
DR InterPro; IPR003661; His_kinA.
DR InterPro; IPR005467; His_kinase.
DR InterPro; IPR001789; Response_reg.
DR Pfam; PF03924; CHASE; 1.
DR Pfam; PF02518; HATPase_c; 1.
DR Pfam; PF00512; Hiska; 1.
DR Pfam; PF00072; response_reg; 1.
DR PRINTS; PR00344; BCRLSENSOR.
DR ProDom; PD000039; Response_reg; 1.
DR SMART; SM00387; HATPase_c; 1.
DR SMART; SM00388; Hiska; 1.
DR SMART; SM00448; REC; 1.
DR PROSITE; PS0839; CHASE; 1.
DR PROSITE; PS0109; HIS_KIN; 1.
DR PROSITE; PS0110; RESPONSE_REGULATORY; 1.
KW Kinase; Phosphorylation; Sensory transduction.
SQ SEQUENCE 974 AA; 108074 MW; 3EF67B020D839F0 CRC64;
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Query Match 50.1%; Score 2705.5; DB 10; Length 974;

Best Local Similarity 57.9%; Pred. No. 4.4e-168;

Matches 562; Conservative 136; Mismatches 211; Indels 61; Gaps 16;

Qy 111 WIIIVGFTSSGIYQW-----MDDANKRRREVLVSMCDQARMLQDQFSVNVHVALA 164

Db 22 W-VLTAVCSAWEHTLRDSMD-----RAERLVSMCEERARMLEQFGVTVNVHVAIA 75

Qy 165 ILVSTFHYKNPSAIDQETFAETARTAFERPLISGVAYABKVNFEREMFERQHNWVIX 224

Db 76 ILISTFNEKSPPAIDQDTFAKTARTSFERPLLVGFAQVRVHEREMFESQGGWVN 135

Qy 225 TMDRGSPVDEYAPVIFPSQDSVSYLSLDMGGEEDRENILRARETGKAVLTPPRL 284

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Db 136 TMQR-EPAPPOVEYAPVIFPSQDTSVYLARIDMMSGEEDRENIFRARTTGKAVLTPPRL 194
Qy 285 ETHELGVLTTPPVYKSSLPENPTYEERIAATAGYILGAFDVESLVENLLGOLAGNAIVV 344
Db 195 GSNHGLVLTFAVYRPLPADASVEQVRVEATIGYLGAFDVESLVENLLSKLAGNQDIVV 254
Qy 345 HYYDITWASDPLVMYGNQDEADRSLSHESKLDGDPFRKHMI CRTHQKAPIPLNVLT 404
Db 255 NYDVTNASDAMVLYGFSLSDEQVFFLHVSMLDGFDFRKHMCRCYRQKLPMPWSAITN 314
Qy 405 VPLEFAIGFLVGYILYGAAMHIVKVEDDFHEMQBLKVRABAAADVAKSQFATVSHERTP 464
Db 315 PLCTFVIMLLGYISIAAAYSRYDKVTEDCRKMEELKTAQEAADVAKSQFLATAHEIRTP 374
Qy 465 MNGILMLMLDLTSLTSQDYAQTACVCGKALIALINEVLDRAKIEAGKLELESVPFD 524
Db 375 MNGVLGMLDMLLTGTLTMTQKYAQTACMCGRALITLINDVLDRAKIEAGKLEAVPFD 434
Qy 525 IRSILDDVLSLFPSESRNKGIELAVFVSDKPEIVKGDGRFROIINLVGNSVKFTEKG 584
Db 435 LRSLMDDVVSLSFSSKREKICIELAVFVCDNVPKYVIGDPWRFRQIILTNLVGNVAKFTERG 494
Qy 585 HIFVKVHLAEQSKDESEP--KNALNGGVSEEMIVVSKQSSXNTLSGVYEAADGRNSWDFK 642
Db 495 HVFVVCLEANSMEANQVHLGAWG--KGRVSESTANGAFNTLSGFEADRRNSWQYFK 552
Qy 643 HLVSSEQSL-----SEFDISSNVLAMVSIETGIGIPLVACQGRVFMFPMQADSSTR 694
Db 553 LLLSDKESLLDLESNSQSDSRVTLAISIEDTGVGIPLOAQDRVFTFPMQADSSTR 612
Qy 695 NYGTTGIGLSISKCLVELMRGOINFI SRPHIGSTFTWFTAVLEKCDKCSAINHMKKPNVEH 754
Db 613 NYGTTGIGLSISKCLAEIMGQGISFTSPSVGSTFTFSATLKHSHK-DISGDSRSRLTEA 671
Qy 755 LPSFTFGMKAVVDKAPVRAAVTYHMKRLGINVDVTSLSKTAVVAAAAPERNGPSLPTK 814
Db 672 LPTAFKGMKAILVDGPRPVSATVRYHLKRLGILLQVVNNNAVY---KAPFGQNGAAGSR 728
Qy 815 PQLDMILVEKDSWISTEDNSDSEIRLLN---SRITNGNVHHSKPKLALFATNITNEFDRAK 871
Db 729 EKASILFIESDFW---RPETDVQLLNHLREQKNGQI-SDGHKVVLIVT-----SEADKX 779
Qy 872 SAGFADTVIMKPLASMIGACLOQVLEL---RKTRQHPGSSPATLKSLLTGKILV 927
Db 780 YGSIFDIWMCKPIRATSIASSIQLLKVEIAERKDNQ---NRPSFLRSLLVGKNILV 834
Qy 928 DDNIIVNRERVAAGALKKFGAEVVCASGOVALGLLOIHPHTFACPMQDQFQATQ 987
Db 835 DDNKVNRVAAAALKKYGANVSCVSGKDAISLLQPPHFRFDACFMDVQMPMDGFEATGQ 894
Qy 988 IRMEKEAKEK-----TNLEWHLPIILAMTADVIHATYEBCLSKSGMDGVVSKPFE 1036
Db 895 IRQWELKANEERKNKLASIEGSTTAEVHLPLVLTAMTADVIQATYECIKSGMDGVVSKPFD 954
Qy 1037 EENLYKSVAK 1046
Db 955 EEQLYQAVSR 964

RESULT 6
Q9CSU2
ID Q9CSU2 PRELIMINARY; PRT; 1176 AA.
AC Q9CSU2;
DT 01-JUN-2001 (TremBLrel. 17, Created)
DT 01-JUN-2001 (TremBLrel. 17, Last sequence update)
DT 01-MAR-2003 (TremBLrel. 23, Last annotation update)
DE Histidine kinase.
GN AHK2.
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eurosids II; Brassicales; Brassicaceae; Arabidopsis.
OX NCBI_TaxID=3702;
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Db	223	HKDYYDLEALPSPVQSEYAPVIFAQDTVSHVSLDMLSGKEDRENVLRRSSKGVLTA	285
Qy	280	PFRLLETHHLGVLVITFFVYKSSLPENPTVEERIAAATAGYLGGAFDVBSLVENLIGQLAGN	339
Db	283	PFPLIKTNRLGVLITFAVYKRDLPNSATPKERIEATNGYLGGVFDIESLVENLIGQLASK	342
Qy	340	QAIVVHVYDITNASDPLVMYGNQDEBADRSLSHESKLDPGDPPFRKHMI CRYHQKAPIPL	399
Db	343	QTIILVNVYDITNHSQPSMVTG- NVSAD- GLERVSPLIFGDLPLKHEMRCRFKQKPPWPV	400
Qy	400	NVLTVPLFFAIGLVGLYVLAAMHIVKVEDDHEMQLKVRAEAADVAKSQFLATVSH	459
Db	401	LSMVTSGILVIALLVAHIHATVSRHKVEEDCKKQLKKKAAADVAKSQFLATVSH	460
Qy	460	EIRTPMNGILGMLAMDTELSTSTORDYAQTAQVCGKALIALINEVLDRAKIEAGKLELE	519
Db	461	EIRTPMNGVLGMLHMLDTELDVTQDYVRTAQASGRALVSLINEVLDAQIESGKLELE	520
Qy	520	SVPTDIRSLDDVLSLSESRNKGIELAFVSKVPIEIKGDSGRFQIILINLVGNSVK	579
Db	521	EVREDLGILDDVLSLSSQKQGVELAVISORVPMILGDPGRFQILITNLGMSI K	580
Qy	580	FTXGHIHFVKVHLAEQSKDESEPKNALGVGSEEMIVSKQSSYNTLSGYEAAADRNSWD	639
Db	581	FTXGHIHFVTVHLVDLFE SIDGETA-----SSPESTLSGLPVADQRQSW E	626
Qy	640	SPKILVSEBQSLSEFDIS- SNVRLMVSIEDTGIGIPLVAGRVFWPMQADSSSTRNYGG	698
Db	627	NFAFSSNGH--RSFEPSPPDINLIVSVEDTGVGIPVEAQSRIFPTFMQVGPISRTHGG	684
Qy	699	TGIGLSIKCIVELMRGOINPISRPHIGSTFWFTAVLEKCDKCSAINHM-----KKPNVE	753
Db	685	TGIGLSIKCLVGLMKGEIGFSSTPKVGSTPTFTAVFS-----NGMQPAERKNDNQ	736
Qy	754	HLPTFGMKAIYVDKAPVRAAVTRYHMKRLGINVDVTSILKTAVAAAAFERNGSPLPT	813
Db	737	PIFSEFGMKAVVDHPRAPAKVSWYHFQRLGIRVEVVRVEQAL-----HYLKITG----	788
Qy	814	KPQLDMILVEKDSWISTEDDSETRLNSRNTGNVHHKSPKALFATNINSEPDRAKSA	873
Db	789	-TTVMNMIIEQEIW--NREADDIFKKLQK-----DPLFLSPKILILANSVSESSIEALCTG	841
Qy	874	GFADVTMFKPLRSMIGACIQOVLLEKRTQOHPGEGSSPATIKSLITGKKILVDDNIVN	933
Db	842	IDPPIVIVKPLRAEWLAATLQRGIGIREPPQHKGPPLILRLNLLGRKILIVDDNNVN	901
Qy	934	RRVAAGALKKFGAECVWCAESQVAGLGIQIPHTFDACFMDIQMPQMDGFQFATROIRNWEK	993
Db	902	LRVAAGALKKYGADVVCESGIKAISLLKPPHEDFACFMDIQMPQMDGFQFATRIIRDWEE	961
Qy	994	EAKEK-----TNLEWHLPILAMTADTVIATVECLKSGMDGYVSKPPEENLY	1041
Db	962	EMNKIRKNGEALIVENGKTSWHLPVLTAMTADVIQATHEECLKCGMDGYVSKPPEARQLY	1021
Qy	1042	KSAVSKPKNPISPS	1056
Db	1022	REVSFPFN-----SPS	1032
RESULT 9			
Q8L816	PRELIMINARY; PRT; 1041 AA.		
AC	Q8L816		
DT	01-OCT-2002 (TremBirel. 22, Created)		
DT	01-OCT-2002 (TremBirel. 22, Last sequence update)		
DT	01-MAR-2003 (TremBirel. 23, Last annotation update)		
DE	Cytokinin receptor.		

RESULT 9

Q8L816	PRELIMINARY; PRT; 1041 AA.
ID	Q8L816
AC	Q8L816;
DT	01-OCT-2002 (TrEMBLrel. 22, Created)
DT	01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT	01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE	Cytokinin receptor.
GN	CKR1.
OS	Catharanthus roseus (Rosy periwinkle) (Madagascar periwinkle).
OC	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC	Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
OC	Asteridae; lamids; Gentianales; Apocynaceae; Rauvolfioideae; Vinaceae;
OC	Catharanthus.

Db 582 HLADEVKPLDIKDEV---LQSLTLIQDRSTASNTLSGFPVVDWRWSWEKFKNLSCMP 638
Qy 647 EEQSLSEFEDISSNVLMTYSIEDTGIGPLVAGGRVPMFPMQADSTSRNYGCTGIGLSIS 706
Db 639 EE-----SKKILLVTVEDTGGIVYDAQDRIFTFPVQADSTSRKYGTGIGLSIS 690
Qy 707 KCLVELMGOQNFISPRPHIGSTFTFAVLEKCDKCSAINHMKPNVHLPTFKGMKAIV 766
Db 691 KRLVDLVGGEIGFVSEPGTGSTFTSFAAFTKAETITGIT--KWEQYDLAVSEFRLKALV 748
Qy 767 VDAKPVRAAVTRYHMKRLGINVDVVSILKTA-----VAAAFAFRNGSPLPKPOLDMI 820
Db 749 VDEKSIRAEVTRYQLKLEVSVDIASTVEAAVSHLSADVNSASER-----VSMV 798
Qy 821 LVKDSWISTEDNSEIBLN-----SRTNGNVHKKPKALFATNTNTEFEFRAK 871
Db 799 LIDEDWS-----DNETMARVYGLCKSDQTSRPSMGM---NPKIFLLANPKSFSDCIELK 851
Qy 872 SAGFADTVIMKPLRASMTGACLOQVLELRKTRQHQPEGSSPATLKSLLTGKILVVDDNI 931
Db 852 STGLVDNVLTPLRLSILISLCQESIGFGRITQ--VTRSNFSTIGNLLKGRMLVVDNDP 909
Qy 932 VNRVAAAGALKKFGAEVVCAESGGVALGLIQTPIHTFDACFMDIQMPQMDGFEATRQIRMM 991
Db 910 VNRVAAELALKYGAVVTCESGAAQLQRLKPPHDFACFMDLQWPNENDGFEATQKIHIL 969
Qy 992 EKEAKEKT-----NLEWHLPILAMTADVIAHTYBECLKSGMDGYVSKPFEEN 1039
Db 970 EREYNENKSGEIGTKSDTDEAYWHTPILAMTADLIQATNEKCRKCGMDGYVSKPFDDEQ 1029
Qy 1040 LYKSAVAKSFK 1049
Db 1030 LYSVAAPFFK 1039

RESULT 10
Q9FZK3
ID Q9FZK3 PRELIMINARY; PRT: 1092 AA.
AC Q9FZK3,
DT 01-MAR-2001 (TrEMBLrel. 16, Created)
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE F17L21.11
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eurosids II; Brassicales; Brassicaceae; Arabidopsis.
OX NCBI_TaxID=3702;
RN [1]
RP SEQUENCE FROM N.A.
RA Johnson-Hopson C., Brooks S., Buehler E., Chao Q., Khan S., Kim C.,
RA Shinn P., Altafi H., Bei Q., Chin C., Chio J., Choi E., Conn L.,
RA Conway A., Gonzales A., Hansen N., Howing B., Koo T., Lam B.,
RA Lenz C., Li J., Liu A., Liu S., Mukharsky N., Nguyen M.,
RA Palm C., Pham P., Sakano H., Schwartz J., Southwick A.,
RA Toriumi M., Vaysberg M., Yu G., Federspiel N.A., Theologis A.,
RA Ecker J.R.;
RT "Genomic sequence for Arabidopsis thaliana BAC F17L21 from chromosome
RT I.",
RL Submitted (APR-1998) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RA Ecker J.R.;
RL Submitted (APR-1998) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RA Ecker J.R.;
RL Submitted (JUN-1998) to the EMBL/GenBank/DBJ databases.
RN [4]
RP SEQUENCE FROM N.A.
RA Ecker J.R.;
RL Submitted (DEC-1998) to the EMBL/GenBank/DBJ databases.
RN [5]

RP SEQUENCE FROM N.A.
RA Ecker J.R.;
RL Submitted (AUG-2000) to the EMBL/GenBank/DBJ databases.
RN [6]
RP SEQUENCE FROM N.A.
RA Cheuk R., Shinn P., Brooks S., Buehler E., Chao Q., Johnson-Hopson C.,
RA Khan S., Kim C., Altafi H., Bei B., Chin C., Chio J., Choi E.,
RA Conn L., Conway A., Gonzales A., Hansen N., Howing B., Koo T., Lam B.,
RA Lee J., Lenz C., Li J., Liu A., Liu S., Mukharsky N.,
RA Nguyen M., Palm C., Pham P., Sakano H., Schwartz J., Southwick A.,
RA Thaveri A., Toriumi M., Vaysberg M., Yu G., Davis R., Federspiel N.,
RA Theologis A., Ecker J.;
RL Submitted (AUG-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AC004557; AAF99730.1; -;
DR InterPro; IPR003594; ATPbind_ATPase.
DR InterPro; IPR004358; Bact_sens_pr_C.
DR InterPro; IPR006189; CHASE.
DR InterPro; IPR003661; His_kinA.
DR InterPro; IPR003467; His_kinase.
DR InterPro; IPR001789; Response_reg.
DR Pfam; PF03924; CHASE; 1.
DR Pfam; PF02518; HATPase_c; 1.
DR Pfam; PF00512; Hiska; 1.
DR Pfam; PF00072; Response_reg; 1.
DR PRINTS; PR00344; BCTRASENSOR.
DR ProDom; PD000039; Response_reg; 1.
DR SMART; SM00387; HATPase_c; 1.
DR SMART; SM00388; Hiska; 1.
DR SMART; SM00448; REC; 2.
DR PROSITE; PS00839; CHASE; 1.
DR PROSITE; PS0109; HIS_KIN; 1.
DR PROSITE; PS0110; RESPONSE_REGULATORY; 1.
DR Phosphorylation; Sensory transduction.
KW Phosphorylation; Sensory transduction.
SQ SEQUENCE 1092 AA; 122824 MW; 72530C55873A216B CRC64;

Query Match 44.5%; Score 2402; DB 10; Length 1092;
Best Local Similarity 48.0%; Pred. No. 3.8e-148;
Matches 528; Conservative 162; Mismatches 257; Indels 154; Gaps 20;

Qy 1 MNWALNNHQBEEPRRIEISDSLENLKSDFYQLGGGALNSSEKPKIDFWR--- 56
Db 25 VSMFVDNGIEDKS---GLLVGVSVDLETK-----MTTLKKKKKKWFWNKISS 69

Qy 57 SGLM--GFAKMQQQQLQHSVAVVMNNNNNDLMGNKKGSTFQEHFALLPKALILIII 114
Db 70 SGLKIPSF-----YQFLGSVKFN-----KAWWRKLVVVMVVF 102

Qy 115 VGFISSGIYQWMDANKIRREEVLSVMSQDQARMLQDQPSVNVHVALAILVSTFHYHK 174
Db 103 WVLVSIWTFYFSQAMEKKEKTLASGCDERARMLQDQFNVMNHVQMSILISTFHHGK 162

Qy 175 NPSAIDQETAEYTAFTAFERPLLSGVAYAEKVYVNERFERQHNWIKTM----- 226
Db 163 IPSAIDQRTSEYTDRTSFERPLTSGVAYAMRVLHSEREFEQQGTIRKNYSLEQNPV 222

Qy 227 -----DRGEPSPVRDEYAPVIFPSQSVSYLSLSDMMGSEEDRENILRARETGKAVLTS 279
Db 223 HKDDYDLEALPEPSQBEYAPVIFAQDVTSHVSVSLDMLSGKEDRENIVRARSSGKVLTA 282

Qy 280 PFRLLETHHLGVLTTPFYKSSLPENPTVEERATAAGYLGGAFFDVESLVENLGLQAGN 339
Db 283 PFPLIKTNRLGVLTTPFAVYKRDLPFSNATPKERIEATNGYLGGVDFIESLVENLQQLASK 342

Qy 340 QAIWVHVYDITNASDPLVMYGNODEADRSLSHESKLDGDPFRKHKM----- 387
Db 343 QTIWVYDITNHSQIPISMYGT-NVSGD-GLERVSPLIFGDPRLKHEMRCRYQLAHTYV 400

Qy 388 -----ICRYHQKAPITPLNVLTTVPLFFAIGFVIGVILYGAAMHIV 427
Db 401 CNFFLPARIQVLTFCCELLPLCRFKQKPPWVLSWVTSFGILVIALVAHIHATVSRIH 460

Qy 428 KVDEDDHEMOELKVRAEADVAKSQFLATVSHIRTPMNGILGMLAMLLDTLSSTORDY 487
Db 428 KVDEDDHEMOELKVRAEADVAKSQFLATVSHIRTPMNGILGMLAMLLDTLSSTORDY 487

Db 461 KVEEDCDKMKQKKKAEADVAKSQFLATVSHIRTPMNGVGLMHLMDTELDVTQDDY 520
QY 488 AQTAAQCGKALIALINEVLDRAKIEAGKLELESVPFDIRSLDDVLSLSESRNKGIHL 547
Db 521 VRTAAQAGRALVSLINEVLDQAKIESGKLELEVRFDLGLDLDVLSLSSKQKGVEL 580
QY 548 AVFVSDKVEIIVKDGSRFRQIIINLVGNSVKTEKGHIFVKVHLAEQSKDESEPKNALN 607
Db 581 AVTISRVPDMLGDRFRQIIINLVGNSVKTEKGHIFVKVHLAEQSKDESEPKNALN 638
QY 608 GGVSEEMIVVSKOSSYNTLISGYEAAAGRNWSDFKHLVSEEQSLSEFDSIS-SNVRMLVSI 666
Db 639 -----SSPSTLSGLPVADRQRWENFKAFSSNGH--RSFSPPPDINLIVSV 684
QY 667 EDTGIGIPLVAQGRVMPFQAQSDTSRNYGGTIGLISKICLVLMRGQINFSRPHIG 726
Db 685 EDTGVGIPVEAQSRITFPFQVGPISIRTHGGTIGLISKICLVLMRGQINFSRPHIG 744
QY 727 STWFTAVLEKDKCSAINHM-----KKPNVEHLPTSTFGKMAIIVDAKPVRAAVTRYHM 781
Db 745 STFTTAVFS-----NGMQPAERKNDNNQPIFSEFRGMKAVVVDHRPARAKVSWYHF 796
QY 782 KRIGINVDVYSLKTAIVAAAEERNGSPPLTKPQDMLILVEKDSWISTEDNDSIRLLN 841
Db 797 QRLGIRVEVPRVEQAL-----HYLKGIT-----TTVMMLIEQIHW--NREADDIFKKLQ 845
QY 842 SRINGNVHHSKPLALFATNITSEFDRKASAGFADTIVIMPLRASMIGACLOQVLELR 901
Db 846 K-----DPLFLSPKILLANSVSESSIBALCTGIDPPVIVKPLRSMALATLQRLGIGI 901
QY 902 TROQHEGSPATLKSLLTGKILVDDNINVRRAAGALKKFGAEVVCVCAESQVAGLL 961
Db 902 REPPQKHGPPALLIRNLLGKILVDDNINVRRAAGALKKFGAEVVCVCAESQVAGLL 961
QY 962 QIPHTFDACFMDIQMPQMDGFATROIRMEKEAKEK-----TNLSWHLPIILA 1009
Db 962 KPHEFDACFMDIQMPQMDGFATROIRMEKEAKEK-----TNLSWHLPIILA 1009
QY 1010 MTADVIAHYECLKSGMDGY 1030
Db 1022 MTADVIAHYECLKSGMDGY 1042

RESULT 11

Q8RYG4 PRELIMINARY; PRT; 1023 AA.
AC Q8RYG4;
DT 01-JUN-2002 (TrEMBLrel. 21, Created)
DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Putative histidine kinase.
GN P0592G05.13.
OS Oryza sativa (japonica cultivar-group).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC Ehrhartoideae; Oryzoideae; Oryza.
OX NCBI_TaxID=39947;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=cv. Nipponbare;
RA Sasaki T., Matsumoto T., Yamamoto K.;
RT "Oryza sativa (japonica cultivar-group) genomic DNA, chromosome 1, PAC
clone:P0592G05."
RL Submitted (JAN-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL: AP004672; BAB90827.1; -.
DR Gramineae; Q8RYG4;
DR InterPro: IPR003594; ATPbind_ATPase.
DR InterPro: IPR006189; CHASE.
DR InterPro: IPR003661; His_kinase.
DR InterPro: IPR005467; His_kinase.
DR InterPro: IPR001789; Response_reg.
DR Pfam: PF03924; CHASE; 1.
DR Pfam: PF02518; HATPase_c; 1.

DR Pfam: PF00512; HisKA; 1.
DR Pfam: PF00072; response_reg; 1.
DR ProDom: PD00039; Response_reg; 1.
DR SMART: SM00387; HATPase_c; 1.
DR SMART: SM00388; HisKA; 1.
DR SMART: SM00446; REC; 1.
DR PROSITE: PS00839; CHASE; 1.
DR PROSITE: PS0109; HIS_KIN; 1.
DR PROSITE: PS0110; RESPONSE_REGULATORY; 1.
KW Kinase; phosphorylation; sensory transduction.
SQ SEQUENCE 1023 AA; 113219 MW; 469AC35146CDF62B CRC64;

Query Match 44.0%; Score 2375; DB 10; Length 1023;
Best Local Similarity 51.6%; Pred. No. 2e-146;
Matches 508; Conservative 154; Mismatches 229; Indels 94; Gaps 21;

QY 108 LLLMLIIIVGFISSGIIQWMDANKIRREBVLVSMCDQARMLODQPSVSNVHVALIIV 167
Db 84 LLLMLIAGSLGSIYFLFMAQSLDKRDSLSMCDERARMLQDQPNVSMNHLOALAIIV 143
QY 168 STFVHKNPASIDQETFAEYRTARTAFERPLLSGVAYAEKVNFRFEMPERQHNWIKTW- 226
Db 144 STFHSKTSASIDQMTFAEYRTARTAFERPLTSGVAYAVVTHGEREQFERQQGWAIKOMY 203
QY 227 -----DRGEPSP-----VR-----DEYAPVIFQDSVSVSYLESMDMSGEEDRENILRA 269
Db 204 SSSNKKQSPGPGPGDAVAEIREPAEYAPVIFAQDAYKHVISTFMDLSGNEEDRONILRA 263
QY 270 RETGAVLTSPRLLETHLGVVLAFFPVYKSSLPENPTVEERIAATAGVLCGAFVSVIIV 329
Db 264 RKSQGGVLTAPPKLL--NNRLGVILTYTVKYSELPAYARPHERIQAAGVILGGIFDIQALV 322
QY 330 ENLLGQAGNQAIIVHVVDITNASDPLVMYGNQDEADRSLSHESKLDGDFPRKHMTIC 389
Db 323 EXLLKQLASQESIMWNYDTTNE--PISMYG--DDTSGMCHSVSVINFGDSRKHMEHC 378
QY 390 RTHQKAPILANLVTVPLFFAIGFLVGYILYGAAMHIVKVEDDFHEMOBLKVAEADVA 449
Db 379 RFEKPPWPWLAISSFGTLVIALTLTGHIQATVHRIAKVEDDFHMKSELKKRAEDADVA 438
QY 450 KSQFLATVSHERTPMNGILGMLMLDTELSSTORDYATQATQVCGKALIALINEVLDRA 509
Db 439 KSQFLATVSHERTPMNGVGLMQLMDTDLDTTQDYVYRTAQASGKALVSLINEVLDQA 498
QY 510 KTEAGKLELESVPFDIRSLDDVLSLSESRNKGIELAVFYSDKVPETVKGDSGRFROI 569
Db 499 KTESGKLELETVPFDLRTVCCDILSLFCGKAEKGLAVYVSDQVQFQILIGDPRGIRI 558
QY 570 IINLVGNSVKTEKGHIFVKVHLAEQSKDESEPKNALNGVSEEMIVVSKQSSYNTLSGY 629
Db 559 ITNLVGNISIKFTERGHIVLTVHWBEVMSCLEVETGI-----QNTNLTSGY 604
QY 630 EAADGNSWDSF-----KHLVSEEQSLSEFDSISNVRMLVSIEDTGIGIPLVAQGRVMPF 685
Db 605 PVANRCSWESIRLFRNLEHSEKSFAP--ASDSISLVSIVSDTGVGIPFEAQSVFTPF 663
QY 686 MQADGSTSRNYGGTIGLISKICLVLMRGQINFSRPHIGSTFWFTAVLEKDKCSAIN 745
Db 664 MQVGPRIARHGGTIGLISKICLVLMRGKELGAFASKPHVSGTFTFTAVLMRA----- 716
QY 746 HMKKNVNEHLPTFGKMAIIVDAKPVRAAVTRYHMKRIGINVDVYSLKTAIVAAAPAE 805
Db 717 HCKGNDIK--SSEFGKINALVVDHRPARAKVTKYHLQRLGVKTELTAELNQFI-----SK 769
QY 806 RNSGPLTPKQDMLILVEKDSWISTEDNDSIR--LLNSRTNGNVHHSKPLALFATNITN 864
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QY 865 SFDRKASAGFADT-----VIMKPLRASMIGACLOQV--ELRTR--QQHEGSGSPATL 915
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Db      873  G S L L H K Q I I V D D N I V N L K V A A G A L K Y G A V T C A D S G K K A I T L L P P H N F D A C F M D I Q 932
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Qy      1025  S G M D G Y V K P E E E N I Y S V A K S P K 1049
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RESULT 12
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ID Q8S6P5 PRELIMINARY; PRT; 925 AA.
AC Q8S6P5;
DT 01-JUN-2002 (Tremblrel. 21, Created)
DT 01-JUN-2002 (Tremblrel. 21, Last sequence update)
DT 01-MAR-2003 (Tremblrel. 23, Last annotation update)
DE Putative histidine kinase.
GN OSJNB0073L01.1.
OS Oryza sativa (japonica cultivar-group).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC Ehrhartoideae; Oryzaeae; Oryza.
OX NCBI_TaxID=39947;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=cv. Nipponbare;
RA Buell C.R., Yuan Q., Ouyang S., Liu J., Gansberger K., Kim M.M.,
RA Overton II L.L., Bera J.J., Tsitrin T., Krol M.I., Jarrahi B.B.,
RA Jin S.S., Koo H., Zismann J.V., Hsiao J., Blunt S., Vanaken S.B.,
RA Uterback T.T., Feldblyum T.V., Yang Q.Q., Haas B.J., Suh B.B.,
RA Peterson J.J., Quackenbush J., White O., Salzberg S.L., Fraser C.M.;
RT "Oryza sativa chromosome 10 BAC OSJNB0073L01 genomic sequence.";
RL Submitted (Apr-2002) to the EMBL/GenBank/DBSJ databases.
DR EMBL; AC092548; AM18726.1; -.
DR Gramene; Q8S6P5; -.
DR InterPro; IPR003594; ATPbind_ATPase.
DR InterPro; IPR006189; CHASE.
DR InterPro; IPR003661; His_kinA.
DR InterPro; IPR005467; His_kinase.
DR InterPro; IPR001789; Response_reg.
DR Pfam; PF03924; CHASE; 1.
DR Pfam; PF02518; HATPase_c; 1.
DR Pfam; PF00512; Hiska; 1.
DR Pfam; PF00072; response_reg; 1.
DR ProDom; PD000039; Response_reg; 1.
DR SMART; SM00387; HATPase_c; 1.
DR SMART; SM00388; Hiska; 1.
DR SMART; SM00448; REC; 1.
DR PROSITE; PS50839; CHASE; 1.
DR PROSITE; PS0109; HIS_KIN; 1.
DR PROSITE; PS0110; RESPONSE_REGULATORY; 2.
KW Kinase; Phosphorylation; Sensory transduction.
SQ SEQUENCE 925 AA; 102928 MW; 6046D9AC28824219 CRC64;

Query Match 41.7%; Score 2248.5; DB 10; Length 925;
Best Local Similarity 52.4%; Pred. No. 3.2e-138;
Matches 495; Conservative 144; Mismatches 223; Indels 83; Gaps 20;

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Qy      193  F E R L L S G V A E K V N F E R M F R O H N W I K T M - - - - - D R G E P S P V R E Y A 239
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RESULT 13
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ID Q8GUG0 PRELIMINARY; PRT; 652 AA.
AC Q8GUG0;
DT 01-MAR-2003 (Tremblrel. 23, Created)
DT 01-MAR-2003 (Tremblrel. 23, Last sequence update)
DT 01-MAR-2003 (Tremblrel. 23, Last annotation update)
DE Histidine kinase-like protein.
GN AT5G35750.
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eurosids II; Brassicales; Brassicaceae; Arabidopsids.
OX NCBI_TaxID=3702;
RN [1]
RP SEQUENCE FROM N.A.
RA Southwick A., Nguyen M., Tripp M., Palm C.J., Jones T., Wu T.,
RA Carninci P., Chen H., Cheuk R., Chan M.M., Chang C.H., Dale J.M.,
RA Deng J.M., Hayashizaki Y., Hsuan V.W., Lee J.M., Ishida J., Kamiya A.,
RA Kawai J., Kim C.J., Narusaka M., Oncidera C.S., Quach H.L., Sakurai T.,

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: November 28, 2003, 13:58:18 ; Search time 39.5984 Seconds
(without alignments)
4236.886 Million cell updates/sec

Title: US-09-918-508-6

Perfect score: 5397

Sequence: 1 MWALNNHQEEBPRRIEL.....ENLYKSVAKFKNPISPSS 1057

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1107863 seqs, 158726573 residues

Total number of hits satisfying chosen parameters: 1107863

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : A Geneseq 19Jun03.*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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1	5397	100.0	1057	23	ABG70783
2	5387	99.8	1057	23	AAO22558
3	5387	99.8	1057	24	AAE33694
4	5383	99.7	1057	23	AAO22570
5	5382	99.7	1057	24	AAE33696
6	5379	99.7	1057	24	AAE33695
7	2865	53.1	600	23	ABB91688
8	2546	47.2	1132	21	AAG47090
9	2546	47.2	1176	21	AAG47089

10	2546	47.2	1176	23	ABG70781
11	2546	47.2	1176	24	AAE33692
12	2546	47.2	1238	21	AAG47088
13	2534.5	47.0	1173	23	AAO22568
14	2534.5	47.0	1173	23	ABB93625
15	2485	46.0	1036	23	ABG70782
16	2485	46.0	1036	24	AAE33693
17	2402	44.5	1092	23	AAO22567
18	2402	44.5	1092	23	ABB91150
19	1434	26.6	289	23	AAO22563
20	1415	26.2	274	23	AAO22561
21	1248	23.1	412	21	AAE33694
22	993	18.4	426	21	AAE33695
23	702	13.0	2150	23	AAO22566
24	668	12.4	1081	20	AAE33696
25	664	12.3	1081	20	AAW81600
26	661	12.2	132	23	AAO22564
27	654	12.1	1298	19	AAW68522
28	654	12.1	1298	20	AAV28481
29	652	12.1	1281	20	AAV28484
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35	594.5	11.0	922	22	AAE33695
36	588.5	10.9	922	22	AAE33696
37	585	10.8	1018	21	AAE33697
38	577.5	10.7	816	21	AAE33698
39	571.5	10.6	950	23	ABG93422
40	571	10.6	1122	23	ABG92150
41	551	10.2	105	23	AAO22559
42	541	10.0	747	24	ABU03033
43	531.5	9.8	1146	20	AAW86007
44	517	9.6	185	21	AAE33699
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ALIGNMENTS

RESULT 1

ID ABG70783 standard; Protein; 1057 AA.

XX ABG70783;

DT 09-DEC-2002 (first entry)

DE A. thaliana cytokinin receptor, CRE1, protein.

XX CRE1; plant; antagonist; agonist; cytokinin receptor;
KW receptor; signal transduction; histidine kinase; hormone;
KW cell differentiation; agriculture; growth regulator; harvest.

XX Arabidopsis thaliana.

XX EPI241182-A2.

PD 18-SEP-2002.

XX 13-MAR-2002; 2002EP-0005749.

PR 15-MAR-2001; 2001JP-0073812.

PR 29-JUN-2001; 2001JP-0198639.

XX 29-JUN-2001; 2001JP-0198640.

PA (SUMO) SUMITOMO CHEM CO LTD.

XX Kakimoto T, Higuchi M, Inoue T;

XX WPI; 2002-693041/75.

DR N-PSDB; ABS54452.

A. thaliana cytokinin
Arabidopsis thaliana
Wooden leg (WOL) g
Herbicidally activ
A. thaliana cytokinin
Arabidopsis thaliana
Wooden leg (WOL) g
Herbicidally activ
Wooden leg (WOL) g
Wooden leg (WOL) g
Wooden leg (WOL) g
Eucalyptus grandis
Eucalyptus grandis
Wooden leg (WOL) g
cos-1 histidine ki
Candida albicans C
Wooden leg (WOL) g
N. crassa osp pro
osp1p amino acid s
osp1 histidine ki
osp1 histidine ki
Wooden leg (WOL) g
Candida albicans h
Candida albicans h
Histidine protein k
Histidine protein k
Histidine protein k
Eucalyptus grandis
Eucalyptus grandis
Herbicidally activ
Herbicidally activ
Wooden leg (WOL) g
Moss lipid metabol
Histidine kinase C
Pinus radiata cell
Pseudomonas aerugi

XX Analyzing agonist or antagonist activity of a substance for use as a
PT plant growth regulator, comprises measuring intracellular signal
PT transduction from a cytokinin receptor expressed in a cell contacted
PT with the test substance -
XX
PS
XX Claim 1; Page 39-41; 47pp; English.
XX The invention discloses a method for analysing antagonist or agonist
CC activity to a cytokinin receptor. The method comprises bringing a
CC candidate substance into contact with a transformed cell, in which a DNA
CC encoding the receptor has been introduced, and then measuring the
CC existence, or the quantity, of the intracellular signal transduction from
CC the receptor expressed in the cell. The cytokinin receptor comprises an
CC extracellular region of the receptor, transmembrane regions, a histidine
CC kinase region and a receiver region of the kinase. The transmembrane
CC regions and kinase region are homogeneous to each other and the receptor
CC region is heterogeneous to them. Cytokinins are plant hormones relevant
CC to cell division and differentiation of higher plants. The method is used
CC for analysing agonist or antagonist activity to a cytokine receptor. A
CC substance with agonist or antagonist activity to the receptor can be
CC used, in agriculture, as a plant growth regulator, e.g. after harvest.
CC The advantage is that the candidate substances do not need to be prepared
CC in such large amounts as in previous methods and that the method avoids
CC the immensely long time to observe and evaluate the growth of the plant
CC and the physiological changes of the plant after spraying. The sequence
CC presented is the A. thaliana cytokinin receptor, CRE1, protein.
XX
SQ Sequence 1057 AA;
Query Match 100.0%; Score 5397; DB 23; Length 1057;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1057; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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DB 301 SLPENPTVEERAAATAGYLGGAFDVESLVNLLGQAGNOAIVWHYDITNADSLVMYG 360
QY 361 NODEEADRSLSHESKLDGDFGPPRKHMI CRYHOKAPIPLNVLTTVPLFAIGFLVGYILY 420
DB 361 NODEEADRSLSHESKLDGDFGPPRKHMI CRYHOKAPIPLNVLTTVPLFAIGFLVGYILY 420
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DB 421 GAAMHIVKVEDDPHEMQELKVRAEAAADVAKSQFLATVSHIEIRTPMNGILGLMLLDTEL 480
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DB 781 MKRLGINVDVTSKTA VAAAFERNKSPPTKPDMLVVEKDSWISTENDNDSEIRLL 840
QY 841 NSRTNGNVHHSKPKLALFATNITSEFDRKASAGFADTVIMKPLRASMIGACLOQVLEIR 900
DB 841 NSRTNGNVHHSKPKLALFATNITSEFDRKASAGFADTVIMKPLRASMIGACLOQVLEIR 900
QY 901 KTRQHPGSGSPATLKSLLTGKILVDDNIVNRRVAAGALKKFGAEVVCESGQVALGL 960
DB 901 KTRQHPGSGSPATLKSLLTGKILVDDNIVNRRVAAGALKKFGAEVVCESGQVALGL 960
QY 961 LQIPHTFDACFMDIOMPDQMGFEATRQIRMMEKEAKETNLEWHLPILAMTADVIHATYE 1020
DB 961 LQIPHTFDACFMDIOMPDQMGFEATRQIRMMEKEAKETNLEWHLPILAMTADVIHATYE 1020
QY 1021 ECLKSGMDGYYSKPFEEENLYKSVAKSPKPNPISPSS 1057
DB 1021 ECLKSGMDGYYSKPFEEENLYKSVAKSPKPNPISPSS 1057
RESULT 2
AAO22558
ID AAO22558 standard; Protein; 1057 AA.
XX
AC AAO22558;
XX
DT 28-OCT-2002 (first entry)
XX
DE Wooden leg (WOL) gene related protein SEQ ID No 5.
XX
KW Wooden leg; WOL; vasculature; transgenic plant; agronomic; longer root;
KW wood production; plant; promoter; tree; crop plant.
OS Arabidopsis thaliana.
XX
PN WO200244337-A2.
XX
PD 06-JUN-2002.
XX
PF 29-NOV-2001; 2001WO-US45053.
XX
PR 29-NOV-2000; 2000US-253739P.
XX
PA (UYNV) UNIV NEW YORK STATE.
PA (HELA/) HELARIUTTA Y.
PA (MAHO/) MAHONEN A P.
PA (BONK/) BONKE A W M.
PA (KAUP/) KAUPPINEN L.
PA (RIIK/) RIIKONEN M.
XX
PI Helariutta Y, Mahonen AP, Bonke AWM, Kauppinen L, Riikonen M;
PI Benfey PN;
XX
DR WPI; 2002-599423/64.
XX
PT Novel isolated polypeptide (WOODEN LEG) with ability to regulate a set
PT of asymmetric cell divisions that establish vascular tissue in root and
PT hypocotyl development, useful for improving agronomically valuable
PT plants -

XX	CC	Claim 6; Fig 5D; 187pp; English.	QY	601	EPKVALNGVSEMIYVSKQSSYNTLSGYEADGRNSWDSFKHLVSEEQSLSEFDISSNV	660
PS	CC		Db	601	EPKVALNGVSEMIYVSKQSSYNTLSGYEADGRNSWDSFKHLVSEEQSLSEFDISSNV	660
XX	CC	The invention relates to an isolated WOODEN LRG (WOL) polypeptide, comprising 15 contiguous amino acids of a fully defined Arabidopsis WOODEN LRG protein sequence of 1057 amino acids as given in the CC specification, and to its encoding nucleic acid. The invention also CC relates to an amino acid sequence of domains of protein, e.g., N-terminal CC region, C-terminal domain, etc; or is a naturally occurring allelic CC variant of the above mentioned polypeptide sequence. Expression levels of CC the nucleic acid can be modified to improve the vasculature in transgenic CC plants and enhance the agronomic properties of such plants. Also the WOL CC promoter is used to drive expression of a heterologous coding sequence of CC trees to improve wood production. The WOL nucleic acid may be used as a CC molecular marker for a qualitative trait loci, e.g., longer roots or CC enhanced wood production, in molecular breeding of crop plants. The CC nucleic acid is also useful in DNA amplification assays to identify the CC endogenous WOL genes, WOL mutant alleles and/or WOL expression products CC in cultivars as compared to wild-type plants. They can also be used as CC markers for linkage analysis of qualitative trait loci. The WOL protein CC and/or antibodies can be used as diagnostic reagents in immunoassays to CC detect expression of the WOL gene in cultivars and wild-type plants. The CC WOL protein, its encoding nucleic acid, and its corresponding antibody CC are useful for improving agronomically valuable plants e.g., trees. This CC sequence represents a protein relating to the wooden leg (WOL) protein of CC the invention.	QY	661	RLMVSTEDTGIGPLVAQGRVFMFPMQADSSSTSRNYGGTGIGLSISKCLVELMRGQINFI	720
XX	CC		Db	661	RLMVSTEDTGIGPLVAQGRVFMFPMQADSSSTSRNYGGTGIGLSISKCLVELMRGQINFI	720
XX	CC		QY	721	SRPHIGSTFWFTAVLEKCDKCSAINHMKPNVEHLPSTFKGMKAI VVDKAPVRAAVTRYH	780
PS	CC		Db	721	SRPHIGSTFWFTAVLEKCDKCSAINHMKPNVEHLPSTFKGMKAI VVDKAPVRAAVTRYH	780
XX	CC		QY	781	MKRLGNGVDVTSKTA VAVAAAFAFENGSP LPTKPOLDMILVEKDSWISTEDNDSEIRLL	840
PS	CC		Db	781	MKRLGNGVDVTSKTA VAVAAAFAFENGSP LPTKPOLDMILVEKDSWISTEDNDSEIRLL	840
XX	CC		QY	841	NSRTNGNVHKSPKALFATNITNSFDRKASAGFADVTIMKPLRASMTGACIQQVLELR	900
PS	CC		Db	841	NSRTNGNVHKSPKALFATNITNSFDRKASAGFADVTIMKPLRASMTGACIQQVLELR	900
XX	CC		QY	901	KTRQHPGESSPATLSKLLTGKILVVDNINVRVAAGALKKFGAEVVCABSGQVALGL	960
PS	CC		Db	901	KTRQHPGESSPATLSKLLTGKILVVDNINVRVAAGALKKFGAEVVCABSGQVALGL	960
XX	CC		QY	961	LQIPHTFDACFMDIQMPQMDGFEATQIRMEKEAKEKTNLEWHLPILAMTADVIHATYE	1020
PS	CC		Db	961	LQIPHTFDACFMDIQMPQMDGFEATQIRMEKEAKEKTNLEWHLPILAMTADVIHATYE	1020
XX	CC		QY	1021	ECLKSGMDGVSKPPEENLYKSVAKSPKNPISPSS	1057
PS	CC		Db	1021	ECLKSGMDGVSKPPEENLYKSVAKSPKNPISPSS	1057
XX	CC		QY	1057	AAE33694 standard; Protein; 1057 AA.	
PS	CC		Db	1057	AAE33694 standard; Protein; 1057 AA.	
XX	CC		QY	1057	AAE33694; 16-APR-2003 (first entry)	
PS	CC		Db	1057	AAE33694; 16-APR-2003 (first entry)	
XX	CC		QY	1057	Arabidopsis thaliana histidine kinase 4 (AHK4)-WOL, CRE1 protein.	
PS	CC		Db	1057	Arabidopsis thaliana histidine kinase 4 (AHK4)-WOL, CRE1 protein.	
XX	CC		QY	1057	Shoot formation; senescence; transgenic; transgenic plant; agriculture; cell proliferation; shoot meristem formation; leaf development; AHK; photosynthesis; histidine kinase; enzyme; CRE1.	
PS	CC		Db	1057	Shoot formation; senescence; transgenic; transgenic plant; agriculture; cell proliferation; shoot meristem formation; leaf development; AHK; photosynthesis; histidine kinase; enzyme; CRE1.	
XX	CC		QY	1057	Chimeric - Arabidopsis thaliana.	
PS	CC		Db	1057	Chimeric - Arabidopsis thaliana.	
XX	CC		QY	1057	WO200299079-A2.	
PS	CC		Db	1057	WO200299079-A2.	
XX	CC		QY	1057	12-DEC-2002.	
PS	CC		Db	1057	12-DEC-2002.	
XX	CC		QY	1057	06-JUN-2002; 2002WO-US18066.	
PS	CC		Db	1057	06-JUN-2002; 2002WO-US18066.	
XX	CC		QY	1057	06-JUN-2001; 2001US-296554P.	
PS	CC		Db	1057	06-JUN-2001; 2001US-296554P.	
XX	CC		QY	1057	(GEO) GEN HOSPITAL CORP.	
PS	CC		Db	1057	(GEO) GEN HOSPITAL CORP.	
XX	CC		QY	1057	Sheen J, Hwang I;	
PS	CC		Db	1057	Sheen J, Hwang I;	
XX	CC		QY	1057	WPI; 2003-140613/13.	
PS	CC		Db	1057	WPI; 2003-140613/13.	
XX	CC		QY	1057	Increasing yield in plant, increasing shoot formation in a plant, or delaying senescence in a plant such as wheat, rice, maize, barley, potato, by using transgenes that regulate cytokinin response	
PS	CC		Db	1057	Increasing yield in plant, increasing shoot formation in a plant, or delaying senescence in a plant such as wheat, rice, maize, barley, potato, by using transgenes that regulate cytokinin response	
XX	CC		QY	1057	Disclosure; Page 80-82; 87pp; English.	
PS	CC		Db	1057	Disclosure; Page 80-82; 87pp; English.	
XX	CC		QY	1057	The present invention relates to a novel method of increasing yield in a plant, increasing shoot formation or delaying senescence in a plant. The method involves introducing into plant cells, a transgene having a B-type	
PS	CC		Db	1057	The present invention relates to a novel method of increasing yield in a plant, increasing shoot formation or delaying senescence in a plant. The method involves introducing into plant cells, a transgene having a B-type	

CC trees to improve wood production. The WOL nucleic acid may be used as a
 CC molecular marker for a qualitative trait loci, e.g., longer roots or
 CC enhanced wood production, in molecular breeding of crop plants. The
 CC nucleic acid is also useful in DNA amplification assays to identify the
 CC endogenous WOL genes, WOL mutant alleles and/or WOL expression products
 CC in cultivars as compared to wild-type plants. They can also be used as
 CC markers for linkage analysis of qualitative trait loci. The WOL protein
 CC and/or antibodies can be used as diagnostic reagents in immunoassays to
 CC detect expression of the WOL gene in cultivars and wild-type plants. The
 CC WOL protein, its encoding nucleic acid, and its corresponding antibody
 CC are useful for improving agronomically valuable plants e.g., trees. This
 CC sequence represents a protein relating to the wooden leg (WOL) protein of
 CC the invention.

XX SQ Sequence 1057 AA;

Query Match 99.7%; Score 5383; DB 23; Length 1057;
 Best Local Similarity 99.7%; Pred. No. 0;
 Matches 1054; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 MNWALNNHQBEEPRRIEISDSLEMLKSSDFYOLGGGALNSSEKPKIDFWRSGLM 60
 DB 1 MNWALNNHQBEEPRRIEISDSLEMLKSSDFYOLGGGALNSSEKPKIDFWRSGLM 60
 QY 61 GFAKMQCQOQLOHSVAVKMNNNNDLMGNKKGSTFIOEHRALLPKALILMIIVGFSS 120
 DB 61 GFAKMQCQOQLOHSVAVKMNNNNDLMGNKKGSTFIOEHRALLPKALILMIIVGFSS 120
 QY 121 GIYQWMDANKIRREVLVSMCDQARMQLQDQFSVNVHVALAILVTFHYKKNPSAID 180
 DB 121 GIYQWMDANKIRREVLVSMCDQARMQLQDQFSVNVHVALAILVTFHYKKNPSAID 180
 QY 181 QETFAEYARTAFERPLISGVAYAEKVNVFREMFERQHNWIKTMDRGESPSPVDEYAP 240
 DB 181 QETFAEYARTAFERPLISGVAYAEKVNVFREMFERQHNWIKTMDRGESPSPVDEYAP 240
 QY 241 VIFSODSVSYLESLOMSGEEDRENILRARETGKAVLTSPPRLLETHLGVVLTPPVYKS 300
 DB 241 VIFSODSVSYLESLOMSGEEDRENILRARETGKAVLTSPPRLLETHLGVVLTPPVYKS 300
 QY 301 SLPENPTVEERIAATAGYLGGAFDVESLVNLLGQAGNOATVHVHYDITNASDPLVMYG 360
 DB 301 SLPENPTVEERIAATAGYLGGAFDVESLVNLLGQAGNOATVHVHYDITNASDPLVMYG 360
 QY 361 NQDEADRSLSHESKLDGDPFRKHMI CRVHQKAPI PLNVLTTPVLPFAIGFLVGILY 420
 DB 361 NQDEADRSLSHESKLDGDPFRKHMI CRVHQKAPI PLNVLTTPVLPFAIGFLVGILY 420
 QY 421 GAAMHIVKVEDDFHEMOELKYRAEADVAKQFLATVSHERTPMNGILGMLMLLDTL 480
 DB 421 GAAMHIVKVEDDFHEMOELKYRAEADVAKQFLATVSHERTPMNGILGMLMLLDTL 480
 QY 481 SSTQDYAQTAVQVCKKALIALINEVLDRAKIEAGKLELESVPFDIRSLDDVLSFSES 540
 DB 481 SSTQDYAQTAVQVCKKALIALINEVLDRAKIEAGKLELESVPFDIRSLDDVLSFSES 540
 QY 541 RNKGIELAVFVSDKVPEIKVSGRFRQIIINLVGNSVKFTEKGHIFVKVHLAQSKDES 600
 DB 541 RNKGIELAVFVSDKVPEIKVSGRFRQIIINLVGNSVKFTEKGHIFVKVHLAQSKDES 600
 QY 601 EPKHALNGVSEEMIVWSQSYNTLSGYEADGNNSWDSPKHLVSEQSISEFDISSNV 660
 DB 601 EPKHALNGVSEEMIVWSQSYNTLSGYEADGNNSWDSPKHLVSEQSISEFDISSNV 660
 QY 661 RLWMSIEDTGIGIPVAGRVFMPMQADSSTSRNYGGTIGLSTSKCLVELMQGINFI 720
 DB 661 RLWMSIEDTGIGIPVAGRVFMPMQADSSTSRNYGGTIGLSTSKCLVELMQGINFI 720
 QY 721 SRPHIGSTFWTAVLEKDKCSAINHMKPNVHLPSTFKGKAIIVDAKVPVAAVTRYH 780
 DB 721 SRPHIGSTFWTAVLEKDKCSAINHMKPNVHLPSTFKGKAIIVDAKVPVAAVTRYH 780
 QY 781 MKRLGINVDVTSUKTAVAAAAAFERNGPSPLTPKQLDMILVEKDSWISTEDNDSEIRLL 840

DB 781 MKRLGINVDVTSUKTAVAAAAAFERNGPSPLTPKQLDMILVEKDSWISTEDNDSEIRLL 840
 QY 841 NSRTNGNVHKSPLKALPATNITSEFDRKASAGFADTVINKPLRASMGACLOQVLELR 900
 DB 841 NSRTNGNVHKSPLKALPATNITSEFDRKASAGFADTVINKPLRASMGACLOQVLELR 900
 QY 901 KTRQHPGSGSPATLKSLLTGKILVDDNIVNRVAAAGALKKFGAEVVCASGQVALGL 960
 DB 901 KTRQHPGSGSPATLKSLLTGKILVDDNIVNRVAAAGALKKFGAEVVCASGQVALGL 960
 QY 961 LOIETHTFDACFMDIQMPOMDGFETQIRMEKEAKEKTNLEWHLPILAMTADVHIATYE 1020
 DB 961 LOIETHTFDACFMDIQMPOMDGFETQIRMEKEAKEKTNLEWHLPILAMTADVHIATYE 1020
 QY 1021 ECLSGMDGYVSKPFEENLYKSVAKSPKPNPISPSS 1057
 DB 1021 ECLSGMDGYVSKPFEENLYKSVAKSPKPNPISPSS 1057
 RESULT 5
 AAE33696
 ID AAE33696 standard; Protein; 1057 AA.
 AC AAE33696;
 XX
 DT 16-APR-2003 (first entry)
 XX
 DE Arabidopsis thaliana CRE1 mutant (D973N) protein.
 KW Shoot formation; senescence; transgenic; transgenic plant; agriculture;
 KW cell proliferation; shoot meristem formation; leaf development;
 KW photosynthesis; CRE1; mutant; mutin.
 XX
 OS Arabidopsis thaliana.
 OS Synthetic.
 XX
 FN WO200299079-A2.
 PD 12-DEC-2002.
 XX
 PF 06-JUN-2002; 2002WO-US18066.
 XX
 PR 06-JUN-2001; 2001US-296554P.
 XX
 PA (GEO) GEN HOSPITAL CORP.
 XX
 PI Sheen J, Hwang I;
 XX
 DR WPI; 2003-140613/13.
 XX
 PT Increasing yield in plant, increasing shoot formation in a plant, or
 PT delaying senescence in a plant such as wheat, rice, maize, barley,
 PT potato, by using transgenes that regulate cytokinin response -
 XX
 PS Disclosure; Page 85-87; 87pp; English.
 XX
 CC The present invention relates to a novel method of increasing yield in a
 CC plant, increasing shoot formation or delaying senescence in a plant. The
 CC method involves introducing into plant cells, a transgene having a B-type
 CC response regulator operably linked to a promoter functional in plant
 CC cells to yield transformed plant cells or whose expression reduces the
 CC expression of A-type response regulator in the cells of the plant and
 CC regenerating a plant from the transformed cells. The method is useful
 CC for increasing the yield in a plant, increasing the shoot formation or
 CC delaying senescence in a plant such as wheat, rice, maize, barley,
 CC potato, tomato, soybean, agricultural and commercial purposes including
 CC is useful for variety of agricultural, oat, cotton and sunflower. The method
 CC improving and enhancing photosynthesis, promoting cell proliferation,
 CC shoot meristem formation, promoting leaf development, increasing crop
 CC yields, improving crop and ornamental quality and reducing agricultural
 CC production costs. The present sequence is Arabidopsis thaliana CRE1
 CC mutant protein. This sequence is used to illustrate the method of the

[illegible]

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QY 61 GFAMQOQOQLOHSVAVKMNNDLMGNKKGSTFIOEHRALLPKALILMIIIVGFSS 120
Db 61 GFAMQOQOQLOHSVAVKMNNDLMGNKKGSTFIOEHRALLPKALILMIIIVGFSS 120
QY 121 GIYQMDANKIRREVLVSMCDQARMLOQOFSVNVHVALAILVSTFHYHKNPSAID 180
Db 121 GIYQMDANKIRREVLVSMCDQARMLOQOFSVNVHVALAILVSTFHYHKNPSAID 180
QY 181 QETFAEYRTAFERPLLSGVAYAEBKVNFREMPEROHNVIKTMDRGEPSVRDEYAP 240
Db 181 QETFAEYRTAFERPLLSGVAYAEBKVNFREMPEROHNVIKTMDRGEPSVRDEYAP 240
QY 241 VIFSODSVSYLESIDMMSGEEDRENILRARETGKAVLTSPFRLLETHLGVVLTFFVYKS 300
Db 241 VIFSODSVSYLESIDMMSGEEDRENILRARETGKAVLTSPFRLLETHLGVVLTFFVYKS 300
QY 301 SLPENPTVEERIAATAGYLGAFDVESLVENILGOLAGNQAI VHVYDITNASDPLVMYG 360
Db 301 SLPENPTVEERIAATAGYLGAFDVESLVENILGOLAGNQAI VHVYDITNASDPLVMYG 360
QY 361 NQDEADRSLSHESKLDGDFPRKHMTCRYHQKAPIPLNVLTTPVFFAIGFLVGILY 420
Db 361 NQDEADRSLSHESKLDGDFPRKHMTCRYHQKAPIPLNVLTTPVFFAIGFLVGILY 420
QY 421 GAAMHIVKVEDDFHEMOELKVRAEAADYAKSQFIATVSHIETPMNGILGMLMLDTEL 480
Db 421 GAAMHIVKVEDDFHEMOELKVRAEAADYAKSQFIATVSHIETPMNGILGMLMLDTEL 480
QY 481 SSTORDYAQTAVCGKALIALINEVLDRAKIEAGKLELESVPFDIRSILDVLSLFEES 540
Db 481 SSTORDYAQTAVCGKALIALINEVLDRAKIEAGKLELESVPFDIRSILDVLSLFEES 540
QY 541 RNKGIELAVFVSDKVPETVKGDSGRFRQIIINLVGNSVKFTEKGHI FVKVHLAEQSKDES 600
Db 541 RNKSIELAVFVSDKVPETVKGDSGRFRQIIINLVGNSVKFTEKGHI FVKVHLAEQSKDES 600
QY 601 EPKNALNGVSEEMIVVSKQSYNTLSGYEAADGRNSWDSFKHLVSEBQSLSEFDISNV 660
Db 601 EPKNALNGVSEEMIVVSKQSYNTLSGYEAADGRNSWDSFKHLVSEBQSLSEFDISNV 660
QY 720 RLMTSIEDTGIGIPLVAGRVFMPFMOADSTSRNYGGTGIGLSISKCLVELMGOINFI 720
Db 720 RLMTSIEDTGIGIPLVAGRVFMPFMOADSTSRNYGGTGIGLSISKCLVELMGOINFI 720
QY 780 SRPHIGSTFWFTAVLEKCDKCSAINHMKPNVEHLPSFTFGMKAI VVDKAPVRAAVTRYH 780
Db 780 SRPHIGSTFWFTAVLEKCDKCSAINHMKPNVEHLPSFTFGMKAI VVDKAPVRAAVTRYH 780
QY 840 MKRLGINVDVTSLSKTAVAAAFERNKSPPTKPOLDMILVEKDSWISTEDNDSEIRLL 840
Db 840 MKRLGINVDVTSLSKTAVAAAFERNKSPPTKPOLDMILVEKDSWISTEDNDSEIRLL 840
QY 900 NSRTNGNVHKS PKLALFATNITNSEFDRAKSAGFADTVIMKPLRASMI GACLOQVLELR 900
Db 900 NSRTNGNVHKS PKLALFATNITNSEFDRAKSAGFADTVIMKPLRASMI GACLOQVLELR 900
QY 960 KTRQOHEGSGSPATLSKLLTGKKILVDDNIVNRRVAAGALKKFGAEVVCESQVALGL 960
Db 901 KTRQOHEGSGSPATLSKLLTGKKILVDDNIVNRRVAAGALKKFGAEVVCESQVALGL 960
QY 1020 LQIPHTFDACFMDIQMPQMDGFEATROI RMMEKAKETNLEWHLPILAMTADVIHATYE 1020
Db 961 LQIPHTFDACFMDIQMPQMDGFEATROI RMMEKAKETNLEWHLPILAMTADVIHATYE 1020
QY 1057 ECLKSGMDGVVSKPFEENLYKSVAKSKFNPISPSS 1057
Db 1021 ECLKSGMDGVVSKPFEENLYKSVAKSKFNPISPSS 1057
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RESULT 7
ID ABB91688
XX

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AC ABB91688;
XX 31-MAY-2002 (first entry)
XX Herbicidally active polypeptide SEQ ID NO 899.
XX Herbicidally active polypeptide SEQ ID NO 899.
XX Herbicidal; plant; agriculture; herbicide.
XX Arabidopsis thaliana.
OS WO2002102110-A2.
XX 07-FEB-2002.
XX 28-AUG-2001; 2001WO-EP098992.
XX 28-AUG-2001; 2001WO-EP098992.
XX (FARB ) BAYER AG.
XX Tietjen K, Weidler M;
XX WPI; 2002-269010/31.
XX Identifying plant target proteins for herbicidally active compounds, comprising aligning and comparing nucleic acid or amino acid sequences from plant from plant with nucleic acid or amino acid sequences from non-plant organisms -
XX Claim 5; SEQ ID NO 899; 26lpp + Sequence Listing; English.
XX The invention relates to identifying target proteins (ABB90790-ABB94016) for herbicidally active compounds, comprising aligning and comparing nucleic acid or amino acid sequences from plant with nucleic acid or amino acid sequences from non-plant organisms using suitable search parameters, where plant sequences having an E-value greater by a factor of 3 than the E-value of most similar non-plant sequences are selected. The polypeptides or nucleic acids encoding them are useful for identifying modulators. The identified modulators are useful as herbicides.
XX Sequence 600 AA;
XX Query Match 53.1%; Score 2865; DB 23; Length 600;
XX Best Local Similarity 90.8%; Pred. No. 1e-242;
XX Matches 575; Conservative 0; Mismatches 2; Indels 56; Gaps 2;
QY 424 MHIVKVEDDFHEMOELKVRAEAADYAKSQFIATVSHIETPMNGILGMLMLDTELST 483
Db 1 MHIVKVEDDFHEMOELKVRAEAADYAKSQFIATVSHIETPMNGILGMLMLDTELST 60
QY 484 QRDYAQTAVCGKALIALINEVLDRAKIEAGKLELESVPFDIRSILDVLSLFEESRNK 543
Db 61 QRDYAQTAVCGKALIALINEVLDRAKIEAGKLELESVPFDIRSILDVLSLFEESRNK 120
QY 544 GIELAVFVSDKVPETVKGDSGRFRQIIINLVGNSVKFTEKGHI FVKVHLAEQSKDESPEK 603
Db 121 SIELAVFVSDKVPETVKGDSGRFRQIIINLVGNSVKFTEKGHI FVKVHLAEQSKDESPEK 180
QY 604 NALNGVSEEMIVVSKQSYNTLSGYEAADGRNSWDSFKHLVSEBQSLSEFDISNVRLM 663
Db 181 NALNGV-----NVLRLM 192
QY 664 VSTEDTGIGIPLVAGRVFMPFMOADSTSRNYGGTGIGLSISKCLVELMGOINFI SRP 723
Db 193 VSTEDTGIGIPLVAGRVFMPFMOADSTSRNYGGTGIGLSISKCLVELMGOINFI SRP 252
QY 724 HIGSTFWFTAVLEKCDKCSAINHMKPNVEHLPSFTFGMKAI VVDKAPVRAAVTRYHMKR 783
Db 253 HIGSTFWFTAVLEKCDKCSAINHMKPNVEHLPSFTFGMKAI VVDKAPVRAAVTRYHMKR 312
QY 784 LGINVDVTSLSKTAVAAAFERNKSPPTKPOLDMILVEKDSWISTEDNDSEIRLNSR 843
|||
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Db 1066 KKIASEVSAEMFCFSSHHVPIILAMTADVIQATHEECMKCMDGYVSKPFEEVLIYTA V 1125
QY 1045 AKSFKP 1050
|:|:
Db 1126 ARFFEP 1131
RESULT 9
AAG47089
ID AAG47089 standard; Protein; 1176 AA.
XX AAG47089;
XX
DT 18-OCT-2000 (first entry)
XX
DE Arabidopsis thaliana protein fragment SEQ ID NO: 59313.
XX
KW Protein identification; signal transduction pathway; metabolic pathway;
KW hybridisation assay; genetic mapping; gene expression control; promoter;
KW termination sequence.
XX
OS Arabidopsis thaliana.
XX
PN EPI033405-A2.
XX
PD 06-SEP-2000.
XX
PF 25-FEB-2000; 2000EP-0301439.
XX
PR 25-FEB-1999; 99US-0121825.
PR 05-MAR-1999; 99US-0123180.
PR 09-MAR-1999; 99US-0123548.
PR 23-MAR-1999; 99US-0125788.
PR 25-MAR-1999; 99US-0126264.
PR 29-MAR-1999; 99US-0126785.
PR 01-APR-1999; 99US-0127462.
PR 06-APR-1999; 99US-0128234.
PR 08-APR-1999; 99US-0128714.
PR 16-APR-1999; 99US-0129845.
PR 19-APR-1999; 99US-0130077.
PR 21-APR-1999; 99US-0130449.
PR 23-APR-1999; 99US-0130510.
PR 23-APR-1999; 99US-0130891.
PR 28-APR-1999; 99US-0131449.
PR 30-APR-1999; 99US-0132048.
PR 30-APR-1999; 99US-0132407.
PR 04-MAY-1999; 99US-0132484.
PR 05-MAY-1999; 99US-0132485.
PR 06-MAY-1999; 99US-0132486.
PR 06-MAY-1999; 99US-0132487.
PR 07-MAY-1999; 99US-0132863.
PR 11-MAY-1999; 99US-0134256.
PR 14-MAY-1999; 99US-0134218.
PR 14-MAY-1999; 99US-0134219.
PR 14-MAY-1999; 99US-0134221.
PR 14-MAY-1999; 99US-0134370.
PR 18-MAY-1999; 99US-0134768.
PR 19-MAY-1999; 99US-0134941.
PR 20-MAY-1999; 99US-0135124.
PR 21-MAY-1999; 99US-0135353.
PR 24-MAY-1999; 99US-0135629.
PR 25-MAY-1999; 99US-0136021.
PR 27-MAY-1999; 99US-0136392.
PR 28-MAY-1999; 99US-0136782.
PR 01-JUN-1999; 99US-0137222.
PR 03-JUN-1999; 99US-0137528.
PR 04-JUN-1999; 99US-0137502.
PR 07-JUN-1999; 99US-0137724.
PR 08-JUN-1999; 99US-0138094.
PR 10-JUN-1999; 99US-0138540.
PR 10-JUN-1999; 99US-0138847.
PR 14-JUN-1999; 99US-0139119.
PR 16-JUN-1999; 99US-0139452.
PR 16-JUN-1999; 99US-0139453.
PR 17-JUN-1999; 99US-0139452.
PR 18-JUN-1999; 99US-0139454.
PR 18-JUN-1999; 99US-0139455.
PR 18-JUN-1999; 99US-0139456.
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Qy	116	GFISSGIYQNMDDANK---IRREEVLSMCDORARMLODPFSVNVHVHALIIVSTHY 172
Dd	303	GGVSFSVW-WFWDNTEELIMKRRETLANNCDEARAFLQDPFNVSJHNVHALSVLSTFFHH 361
Qy	173	HKNPASIDQETFAEYTAATAFERPLLGSVAVAEKVVNPEREMFEROHNVWIKT----- 226
Dd	362	GKIPSAIDQRTFEYTERTNTERPLTSGVAVALKVPHEREKFEKGHWAIKKMETEDQT 421
Qy	227	-----DRGSPSPVRDEYAPVIFSQDSVSYLESMDMSGEEDRENILRARBTGKAVLT 279
Dd	422	VVQDCPVENFPDPAIQDEYAPVIFAQTVSHIVSDVMMSGEEDRENILRARASGKVLTS 481
Qy	280	PFRLETHHLGVLTFFPYKSKSLDENPTVEERIAATAGYLGAFPVESLIVENLLQLACN 339
Dd	482	PFKLKSNHLGVLTTFAYDTLSLPDATEQRVEATI GYLGA SYDMP SILVEKXLLHQ LASK 541
Qy	340	QAIVVHVVDITNASDPLVMNGQDEEADRSLSHESKLDGDFGRKHMITCRVHOKAPIPL 399
Dd	542	QTIADVTDTTNTSLIKMYGS--EIGDISQHISSLDFGDPSPRNHEMCHRPKHLPIPW 599
Qy	400	NVLTVTPLFAIGLVGYLYCAAMHI VKVBDDDFHEMOELKVRABAAADVAKSQFLATVSH 459
Dd	600	TAITPSILVLTITVLGVILYEAINRIATVEDCQKRELKARABAADIANSQFLATVSH 659
Qy	460	EIRTPMGILQWLMLDTELSSQTDQDYAQTAQVCVGKALIALINEVLDRAKIEAGKLELE 519

organisms -
PS Claim 5; SEQ ID NO 2836; 261pp + Sequence Listing; English.
XX
CC The invention relates to identifying target proteins
CC (ABB90790-ABB94016) for herbicidally active compounds, comprising
CC aligning and comparing nucleic acid or amino acid sequences from plant
CC with nucleic acid or amino acid sequences from non-plant organisms using
CC suitable search parameters, where plant sequences having an E-value
CC greater by a factor of 3 than the E-value of most similar non-plant
CC sequences are selected. The polypeptides or nucleic acids encoding them
CC are useful for identifying modulators. The identified modulators are
CC useful as herbicides.
XX
XX Sequence 1173 AA;
SQ
Query Match 47.0%; Score 2534.5; DB 23; Length 1173;
Best Local Similarity 52.5%; Pred. No. 4.2e-213; Mismatches 244; Indels 87; Gaps 18;
Matches 538; Conservative 156;
73 HSAVYMNNDLNGNKGSTFIQHRALLPKAL-----ILWIIIV 115
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241 GGVSFVW-WFWDNTNEIIMKRRETLANMCDERARVLOQDFNVSLNHVHALSILVSTFHH 299
173 HKNPSAIDQENPAEYTAFTAFERPLLSGVAAKVNFEREMFERQHNWIKTW----- 226
300 GKIPSAIDQRTFEETETNTERPLTSGVAVALKVPHSERKEFEKHGWAIAKKMETEDQT 359
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340 QAIVVHVYDIITNASDPLVMYGNQDEADRSLSHESKLDGDPFRKHKMICRYHOKAPIPL 399
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718 --ERGHIFISVHLADEVK--EPL-TIEDAVLKQRLALGCSEGETVSGFPAVNAWSWK 771
640 SFKHLVSEEQSLSEFDSNVRLMVSTEDTIGIPLVAQGVFMPFQADSTSRNYGGT 699
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760 KGMKAIYVDKAPVAAVTRHYMKRLGINVDVVTSLKTAVVAATAAFAERNGSPKPKOLDM 819
885 TGLRALVIDNENIRAEVTRVRLRLGTISADIVSLRWACTCISKLEY-----LAM 935
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QY 1046 KSEXP 1050
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XX AC ABG70782;
XX DT 09-DEC-2002 (first entry)
XX DE A. thaliana cytokinin receptor, AHK3, protein.
XX AHK3; plant; antagonist; agonist; cytokinin receptor;
KW receptor; signal transduction; histidine kinase; hormone; cell division;
KW cell differentiation; agriculture; growth regulator; harvest.
OS Arabidopsis thaliana.
XX
FH Key Location/Qualifiers
FT Region 32..1036
FT /note= "This region is specifically claimed in Claim 1"
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XX EPI241182-A2.
PD 18-SEP-2002.
XX 13-MAR-2002; 2002EP-0005749.
XX 15-MAR-2001; 2001JP-0073812.
PR 29-JUN-2001; 2001JP-0198639.
PR 29-JUN-2001; 2001JP-0198640.
XX (SUMO) SUMITOMO CHEM CO LTD.
XX Kakimoto T, Higuchi M, Inoue T;
XX WPI; 2002-693041/75.
DR N-PSDB; ABS54451.
XX
XX Analyzing agonist or antagonist activity of a substance for use as a
XX plant growth regulator, comprises measuring intracellular signal
XX transduction from a cytokinin receptor expressed in a cell contacted
XX with the test substance -
PS Claim 1; Page 32-34; 47pp; English.
XX
CC The invention discloses a method for analysing antagonist or agonist
CC activity to a cytokinin receptor. The method comprises bringing a
CC candidate substance into contact with a transformed cell, in which a DNA
CC encoding the receptor has been introduced, and then measuring the
CC existence, or the quantity, of the intracellular signal transduction from
CC the receptor expressed in the cell. The cytokinin receptor comprises an
CC extracellular region of the receptor, transmembrane regions, a histidine
CC kinase region and a receiver region of the kinase. The transmembrane
CC regions and kinase region are homogeneous to each other and the receptor

